

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	78.5	12.9	332	2	T04484	probable chitinase
2	76.5	12.6	245	2	AD0753	flagellar biosynth
3	76.5	12.6	245	2	S78698	probable export pr
4	75.5	12.4	436	2	B70939	hypothetical prote
5	75.5	12.4	519	2	B87353	hypothetical prote
6	75.5	12.4	635	2	T20910	hypothetical prote
7	74	12.2	768	2	T22758	hypothetical prote
8	73.5	12.1	261	2	G65099	probable pyruvate
9	73.5	12.1	346	2	D75303	conserved hypothet
10	73	12.0	227	2	T04420	ribonuclease (EC 3
11	72	11.8	175	2	T36798	probable transcrip
12	72	11.8	2871	2	A55624	fibrillin-1 precur
13	70.5	11.6	467	2	E95850	probable amino aci
14	70.5	11.6	587	2	T08893	hypothetical prote
15	70	11.5	558	2	I58545	glycan precursor
16	69.5	11.4	424	2	D75330	probable beta-lact
17	69	11.3	324	2	JC2395	Fas antigen precur
18	69	11.3	480	2	B61213	hypothetical prote
19	68.5	11.3	431	1	B63092	conserved hypothet
20	68.5	11.3	484	2	E75138	osmoregulated prol
21	68	11.2	683	2	T00872	probable protein k
22	67.5	11.1	384	1	T46966	diheme cytochrome
23	67.5	11.1	1008	1	GNVUUK	glycoprotein precu
24	67.5	11.1	1013	2	I50615	receptor-type prot
25	67	11.0	319	2	JC4390	bone marrow stroma
26	67	11.0	332	2	AH3572	oligopeptide trans
27	67	11.0	394	2	C36942	hypothetical prote
28	67	11.0	893	2	S51603	receptor-like tyro
29	67	11.0	898	2	S47489	receptor tyrosine

A;Residues: 1-227 <ROG>
A;Cross-references: UNIPROT:O04393; EMBL:AF000940; NID:g2150001; PIDN:AAB58719.1; PID:g2150001
A;Experimental source: cv. Igri
C;Genetics:
A;Introns: 35/3; 87/3
C;Superfamily: Enterobacter ribonuclease
C;Keywords: hydrolase

Query Match 12.0%; Score 73; DB 2; Length 227;
Best Local Similarity 30.0%; Pred. No. 8.2;
Matches 30; Conservative 11; Mismatches 45; Indels 14; Gaps 4;

QY 21 LLRSVAGQAGTAPCSRG-SSWADLDKMDCHACRAPHSDFCIGCAAPAPFRLIW 79
DB 91 LLSSLRAEWPTIACFASDGLQFWAHEWEKHTCAQNLFHEGYF---QTAAPRPAPLLD 147

QY 80 PIL-----GGALSLETVLGLL---SGFLVWRRCRRERS 109
DB 148 ALASAGVAPDGGYVTLVSAVKAIQQGTGFEEVFNDEES 187

RESULT 11
T36798
Probable transcription regulator soxR-like - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21614
A;Accession: T36798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <OLI>
A;Cross-references: UNIPROT:Q9S255; EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEI
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEI:SCI30A.18C

Query Match 11.8%; Score 72; DB 2; Length 175;
Best Local Similarity 27.3%; Pred. No. 8.4;
Matches 36; Conservative 13; Mismatches 47; Indels 36; Gaps 6;

QY 2 ARGSLRLRLILV---LGLWALLRSVAGEQAPGTAP-----CSRGSSWSADLDKMDCA 53
DB 49 ARDALRRVAFVAAQVRGVIPLATIREALAEIPEGTPTEDDWARLSEWSRSELDRIKQL 108

QY 54 SCRAPHSDFCIGCAAPAPFRLIWPIILGGALS-TEVL-----GLLSGFLVWR 102
DB 109 N-RLRDHLTDGIC-----GCLSLCTCVLGNPDPAFGERSAGSRLIVER 151

QY 103 RCRERSSPFPX 114
DB 152 RGSTARGGRAPS 163

RESULT 12
A55624
fibrillin-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55624
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene
A;Reference number: A55624; MUID:95130561; PMID:7829516
A;Accession: A55624
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: UNIPROT:Q61554; GB:I29454; NID:g575509; PIDN:AAAS56840.1; PID:g575510
C;Genetics:
A;Gene: Fbn-1

C;Superfamily: fibrillin; EGF homology
F;I201-I236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;
Best Local Similarity 25.3%; Pred. No. 75;
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36' CSRGSSWSADLDKMD-----CASCRRPHS-----DPCLCG 67
DB 2040 CPFGFSWSSGRRCQDLRMSYCYAKFEGGKCSFKSRNHSKQCCCKALKEGWDGDPCELC 2099
QY 68 AAAPPAPFRLIWPIILGGAL 86
DB 2100 PTEFDEAFRCIPEFGSII 2118

RESULT 13

E95850
Probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95850
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-Kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <KUR>
A;Cross-references: UNIPROT:Q92X93; GB:AL591985; PIDN:CAC48469.1; PID:g15139941; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSYMB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20069
A;Genome: plasmid
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;
Best Local Similarity 26.4%; Pred. No. 25;
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLWL-----ALLRSVAGROA-PGTAPCSRGS-----SWSADLD 47
DB 322 LAIMVSGVWASGETGAVLSAAFEALPG-----YGNLYVTISLALFAFTILGWAYAE 376
QY 48 KMDSCASCRRPHSDFCIGCAAPAPFRLIWPI---LGGALSFP 90
DB 377 KCV-----EYLIGTASA--IPFRIVTWTVAFVFGATLSLDF 409

RESULT 14

C70893
hypothetical protein Rv1069c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
C;Accession: C70893
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Cole, S.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70893

Job time : 40 secs

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-587 <COL>
A:Cross-references: UNIPROT:O53417; GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA1718
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv1069c
C:Superfamily: Membrane protein

Query Match 11.6%; Score 70.5; DB 2; Length 587;
Best Local Similarity 32.1%; Pred. No. 30;
Matches 27; Conservative 3; Mismatches 17; Indels 37; Gaps 5;
QY 68 AAAP-----PAPFRLWPI-----LGGALSLETV-----LGLLSG----- 97
DB 27 AATQTPPEPQPIRSTWIRHTYFTGTAMGLVFWFSMTPLPGRLFGQLVSGICGAPG 86
QY 98 -----FLVW--RRCRRSSPPPX 114
DB 87 YGLGVFAVNLVYMRSHNSPPPP 110

RESULT 15

I56545
glypican precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56545; JCL1281; PC1132
R:Litwack, E.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.
J. Neurosci. 14, 3713-3724, 1994
A:Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-an
A:Reference number: I56545; MUID:94267529; PMID:8207484
A:Accession: I56545
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-358 <RES>
A:Cross-references: UNIPROT:P35053; GB:IL34067; NID:G506416; PIDN:AAA41251.1; PID:G506417
R:Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.
Biochem. Biophys. Res. Commun. 188, 395-401, 1992
A:Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a
A:Reference number: JCL1281; MUID:93038690; PMID:1417860
A:Accession: JCL1281
A:Molecule type: mRNA
A:Residues: 1-20,'T',22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>
A:Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425
A:Experimental source: brain
A:Accession: PC1132
A:Molecule type: protein
A:Residues: 24-55;424-445 <KA2>
C:Superfamily: glypican
C:Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; hepara
P:1-23/Domain: signal sequence #status predicted <SIG>
P:24-530/Product: glypican #status predicted <MAP>
P:531-558/Domain: carboxyl-terminal propeptide #status predicted <CTP>
P:55.486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted
P:79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:399,512/Binding site: carbohydrate (Thr) (covalent) #status predicted
P:530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 11.5%; Score 70; DB 2; Length 558;
Best Local Similarity 37.7%; Pred. No. 32;
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLLVLGLWLA--LLRSVAGEQAPGTAPCGSSNSADLDKMDACR---ARPHSDFC 64
DB 221 RSFVQGLGVASDVVRKVA--QVFLAPECSRA-----VMKLVYCAHCRGVFGARPCPDYC 272
QY 65 ----LGCAA 69
DB 273 RNVLKGCLA 281

Search completed: February 14, 2005, 06:47:35

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:17:38 ; Search time 176 Seconds
(without alignments)
331.688 Million cell updates/sec

Title: US-10-062-831-59
Perfect score: 608
Sequence: 1 MARGSLRLRLLLVLGLWLA.....LSGFLVWRRRRSSPPXP 114

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_spot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	94.1	129	1 FN14 HUMAN	Q9np84 homo sapien
2	454	74.7	129	2 Q80XX9	Q80xx9 rattus norv
3	446	73.4	129	1 FN14 MOUSE	Q9cr75 m tumor nec
4	211	34.7	191	2 Q6P2Q4	Q6p2q4 homo sapien
5	136.5	22.5	120	2 Q6SIX7	Q6six7 xenopus lae
6	93.5	15.4	285	2 Q7ZUG0	Q7zj90 thermus the
7	90	14.8	952	2 Q6ZTA9	Q6zta9 homo sapien
8	88	14.5	184	1 T13C HUMAN	Q96rj3 homo sapien
9	87	14.3	333	2 Q9BZG3	Q9bzg3 homo sapien
10	87	14.3	426	2 Q9BZG2	Q9bzg2 homo sapien
11	85.5	14.1	328	2 Q7B998	Q7b998 xenopus lae
12	84.5	13.9	610	2 Q943G8	Q943g8 oryza sativ
13	80.5	13.2	377	2 Q7SDQ0	Q7sdq0 neurospora
14	79.5	13.1	377	2 Q82N80	Q82n80 streptomyce
15	79	13.0	341	2 Q9N0B3	Q9n0b3 macaca fasc
16	78.5	12.9	219	2 Q8BMI5	Q8bmi5 mus musculu
17	78.5	12.9	332	2 Q42839	Q42839 hordeum vul
18	78.5	12.9	387	2 Q8VD70	Q8vd70 mus musculu
19	78.5	12.9	598	2 Q8P6N1	Q8p6n1 mus musculu
20	78.5	12.9	1208	2 Q8QYTA8	Q8qyta8 mus musculu
21	78	12.8	416	2 Q6N7T8	Q6n7t8 rhodospaudo
22	78	12.8	448	1 FBLS RAT	Q9wvh8 rattus norv
23	77	12.7	291	2 Q749U7	Q749u7 geobacter s
24	77	12.7	448	1 FBLS MOUSE	Q9wvh9 mus musculu
25	76.5	12.6	178	2 Q748L8	Q748l8 geobacter s
26	76.5	12.6	245	1 FLIP SALTY	P54700 salmonella
27	76.5	12.6	245	2 Q825R3	Q825r3 salmonella
28	76.5	12.6	732	2 Q81ZX4	Q81zx4 streptomyce
29	76	12.5	216	2 Q7NRH8	Q7nrh8 chromobacte
30	76	12.5	293	2 Q6S6K2	Q6s6k2 sus scrofa
31	76	12.5	411	2 Q8CXG1	Q8cxg1 oceanobacil

32	75.5	12.4	222	2 Q9QEE6	Q9qee6 indian citr
33	75.5	12.4	391	2 Q66LN8	Q66ln8 rhodobacter
34	75.5	12.4	396	2 Q67UT0	Q67ut0 oryza sativ
35	75.5	12.4	436	2 Q53668	Q53668 mycobacteri
36	75.5	12.4	436	2 Q7U2G8	Q7u2g8 mycobacteri
37	75.5	12.4	449	2 Q7DA65	Q7da65 mycobacteri
38	75.5	12.4	519	2 Q9A9X4	Q9a9x4 caulobacteri
39	75.5	12.4	635	2 Q18288	Q18288 caenorhabdi
40	75	12.3	370	2 Q96KN9	Q96kn9 homo sapien
41	75	12.3	1180	2 Q6Z3M5	Q6z3m5 oryza sativ
42	74.5	12.3	112	2 Q8ZB85	Q8zb85 oryza sativ
43	74.5	12.3	202	2 Q80MP4	Q80mp4 indian citr
44	74.5	12.3	330	2 Q86OW5	Q86ow5 mus musculu
45	74	12.2	548	1 LGT3_MOUSE	Q8k406 mus musculu

ALIGNMENTS

RESULT 1
FN14_HUMAN
ID FN14_HUMAN STANDARD; PRT; 129 AA.
AC Q9NP84; Q9HC50;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member Fn14 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).
GN Name=TNFRSF12A; Synonyms=FN14;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=20216634; PubMed=10751351;
Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,
Testa J.R., Peifley K.A., Winkles J.A.,
"The Fn14 immediate-early response gene is induced during liver
regeneration and highly expressed in both human and murine
hepatocellular carcinomas."
Am. J. Pathol. 156:1253-1261(2000).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
Tanaka S., Sugimachi K.;
"Human homologue of Fn14."
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Uterus;
MEDLINE=238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Tringwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP FUNCTION.
RA MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;
RX Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanelow W.C.,
RT "A novel TNF receptor family member binds TNFAIP3 and is implicated in
RT angiogenesis".
RL Immunity 15:837-846(2001).
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_006519;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC -!- INDUCTION: By FGF-1 and phorbol ester.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF191148; AAF69108.1; -
CC EMBL; AB035480; BAA94792.1; -
CC EMBL; AB035481; BAB17850.1; -
CC EMBL; BC002718; AAO02718.1; -
CC Genbank; HGNC:18152; TNFRSF12A.
CC H-InvDB; HIX0012751; -
CC MIM; 605914; -
CC GO; GO:0006928; P:cell motility; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT superfamily member Fnl4
FT DOMAIN 28 80 Extracellular (potential).
FT TRANSMEM 81 101 Potential.
FT DOMAIN 102 129 Cytoplasmic (potential).
FT REPEAT 36 67 TNFR-Cys (atypical).
FT DISULFID 36 49 Potential.
FT DISULFID 52 67 Potential.
FT VARSPIC 33 67 Missing (in isoform 2).
FT FTID=VSP_006519.
SQ SEQUENCE 129 AA; 13911 MW; BF3DFB9C1E1C448 CRC64;

Query Match 94.1%; Score 572; DB 1; Length 129;
Best Local Similarity 93.9%; Pred. No. 6.1e-47;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVLGLWLLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRRLRLVLGLWLLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAPAPFRLNLPILGALSITFVLGLSGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAPAPFRLNLPILGALSITFVLGLSGFLVWRCRRERSPPPX 114

RESULT 2
Q80XX9 PRELIMINARY; PRT; 129 AA.
ID Q80XX9
AC Q80XX9 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 27, Last annotation update)
DE Type 1 transmembrane protein FNL14 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RA Mueller A.M., Giegerich G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY255102; AAP06753.1; -
DR EMBL; BC060537; AAH60537.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR02212; Fibril-assoc.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match 74.7%; Score 454; DB 2; Length 129;
Best Local Similarity 75.4%; Pred. No. 1.1e-35;
Matches 86; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVLGLWLLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRRLRLVLGLWLLALRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAPAPFRLNLPILGALSITFVLGLSGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAPAPFRLNLPILGALSITFVLGLSGFLVWRCRRERSPPPX 114

RESULT 3
FNL14 MOUSE
ID FNL14 MOUSE STANDARD; PRT; 129 AA.
AC Q9CR75; Q9QZW3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)


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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064377; AAH64377.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 191 AA; 20092 MW; 75B166C4B5F0FA01 CRC64;

Query Match 34.7%; Score 211; DB 2; Length 191;
Best Local Similarity 85.1%; Pred. No. 2.5e-12;
Matches 40; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 68 AAAPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRSSPPX 114
DB 130 AAAPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRCKFTTPI 176

RESULT 5
Q6SIX7
ID Q6SIX7 PRELIMINARY; PRT; 120 AA.
AC Q6SIX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fnl4.
GN Name=Fnl4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Brown S.A.N., Winkles J.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY458020; AAR21225.1; -
SQ SEQUENCE 120 AA; 13295 MW; F5B5D0BBA3F7B4F CRC64;

Query Match 22.5%; Score 136.5; DB 2; Length 120;
Best Local Similarity 33.0%; Pred. No. 2.1e-05;
Matches 36; Conservative 16; Mismatches 50; Indels 7; Gaps 3;

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Masashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuhara Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

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CC -!- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AK126775; BAC86684.1; -.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; ASX hydroxyl S.
DR InterPro; IPR000985; ConA-like lec_g1.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR003129; TSP N.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF02210; Laminin G 2; 2.
DR PRINTS; PR00010; EGFLOOD.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF CA; 5.
DR SMART; SM00282; LamG; 3.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF 1; UNKNOWN_8.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00026; EGF 3; 8.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 952 AA; 99727 MW; F90BC8120FCB6D8B CRC64;

Query Match 14.8%; Score 90; DB 2; Length 952;
Best Local Similarity 30.6%; Pred. No. 3.6;
Matches 33; Conservative 14; Mismatches 37; Indels 24; Gaps 6;

QY 22 LRSVAGE--QAGTAPCSRGSSWSADLDKQMDSCSR-----ARHSDFCLGCA 68
DB 830 LEGLAGQCQVP-TLPC-----EANPCLNGGTCRAAGVSEICNARFSGQCFEAK 880

QY 69 AAP-PAPFLLPPIIGGALS-LTFVLGSLGVVWRRCRRERSPPXP 114
DB 881 GLPLPLPPLLEVAVPACACILLLLGSLGILAAKRRQSEGTSPS 928

RESULT 8
T13C HUMAN STANDARD; PRT; 184 AA.
ID T13C_HUMAN PRT; 184 AA.
AC Q96RJ3.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor
DE 3).
GN Name=TNFRSF13C; Synonyms=BAFFR, BR3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RP FUNCTION.
RX MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;
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GN Name=ACPT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767; DOI=10.1006/geno.2001.6556;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09396.1; -.
DR HSSP; P15309; 1ND6.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 14.3%; Score 87; DB 2; Length 333;
Best Local Similarity 35.3%; Pred. No. 2.8;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCRSGSSWADLCKMDCASCARPHSDFLGCG--AAAPPAPFRLLPILGGALS 87
DB 258 PGCPAPCLGRFYQL-----TAPAPPAHGVSCHGYEAAIPAP---VVPILAGAVA 307

QY 88 LTFVLGLSLGLVWVR-RCRRERSSP 111
DB 308 VLVALSLGLGLLAWRPGCLRALGGP 332

RESULT 10
QYBZG2 PRELIMINARY; PRT; 426 AA.
AC Q9BZG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acid phosphatase.
GN Name=ACPT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767; DOI=10.1006/geno.2001.6556;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09393.1; -.
DR HSSP; P15309; 1ND5.
DR Genew; HGNC:14376; ACPT.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.
SQ SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 14.3%; Score 87; DB 2; Length 426;
Best Local Similarity 35.3%; Pred. No. 3.5;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCRSGSSWADLCKMDCASCARPHSDFLGCG--AAAPPAPFRLLPILGGALS 87
DB 351 PGCPAPCLGRFYQL-----TAPAPPAHGVSCHGYEAAIPAP---VVPILAGAVA 400

QY 88 LTFVLGLSLGLVWVR-RCRRERSSP 111

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DB 401 VLVALSLGLGLLAWRPGCLRALGGP 425
RESULT 11
QYBZG2 PRELIMINARY; PRT; 328 AA.
AC Q76B98;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Death receptor-M2.
GN Name=XDR-M2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB111447; BADI1771.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S-ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN 1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 36586 MW; 3FCD1CCAB8533355 CRC64;

Query Match 14.1%; Score 85.5; DB 2; Length 328;
Best Local Similarity 25.4%; Pred. No. 3.8;
Matches 32; Conservative 11; Mismatches 30; Indels 53; Gaps 6;

QY 35 PCSRGSWS---ADLCKMDCASC---ARPHS-----DFCL 65
DB 72 PCHTGSFSGFTGLDHLCTCLSCRDDQBEVRPCTATQNAECCKRGTYCPDLHPCEVCL 131
QY 66 GCAAAPAPFRLLPW-----ILGALSITFVLGLSGF-----LVWRR 103
DB 132 TCTESCPGHELOFPNCNSDSHCGPAQSGSWIIGVCPILLILLIGLCLCKLKN-- 189
QY 104 CRRRS 109
DB 190 CKDGRS 195

RESULT 12
QYBZG2 PRELIMINARY; PRT; 610 AA.
AC Q943G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative receptor protein kinase.
GN Name=P0046R05.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Salitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osemani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flamm M., Seller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa";
RN Nature 0:0-0(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RN Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ABX01000046; EAA34910.1; --
DR EMBL; BX842624; CAF76227.1; --
DR Hypothetical protein.
SQ Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 42342 MW; 1C923E48C2CB6730 CRC64;

Query Match 13.2%; Score 80.5; DB 2; Length 378;
Best Local Similarity 31.3%; Pred. No. 13;
Matches 38; Conservative 11; Mismatches 45; Indels 25; Gaps 7

QY 15 LGIWLALLRS---VAGEQAPGTAPC-----SRGSSWSADLDKCMDC A-SCRARPHSDFCL 65
DB 1 MGLAAPRKSHQVVAQQIPDTLPAPSQPOSQSETSYALSSVTTATTSATPPLPKL 60
QY 66 GCAAAPAPFRLWLPIL-----GGALSLTFVLGLLSG-----FLVRRCRRRSSP 111
DB 61 LAILKTPTSFSS--PVLATSSSAHSSAVALGIVGVFGFTIIFSFIWRLCRR-RSTP 116

RESULT 14
ID Q82N80 PRELIMINARY; PRT; 377 AA.
AC Q82N80;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SAVI423;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_taxid=33903;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NA-4680;
RC MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shibata T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis; deducing the ability of producing secondary
RT metabolites";
RN Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=NA-4680;

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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:15:59 ; Search time 164 Seconds
(without alignments)
268.846 Million cell updates/sec

Title: US-10-062-831-59
Perfect score: 608
Sequence: 1 MARGSLRLRLRLVGLMLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980a:*
2: Geneseqp1990a:*
3: Geneseqp2000a:*
4: Geneseqp2001a:*
5: Geneseqp2002a:*
6: Geneseqp2003a:*
7: Geneseqp2003bs:*
8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description.
1	608	100.0	114	2	Aaw73409 Human sec
2	572	94.1	129	2	Aaw88506 Human liv
3	572	94.1	129	3	Aay57940 Human tra
4	572	94.1	129	4	Aau03498 Human TWE
5	572	94.1	129	5	Abp61512 Human NF-
6	572	94.1	129	5	Abp719827 Human typ
7	572	94.1	129	6	Ada56889 Human sec
8	572	94.1	129	6	Abu56716 Lung canc
9	572	94.1	129	7	Adc74112 Human sec
10	572	94.1	129	7	Adc37867 Human sec
11	572	94.1	129	7	Add89033 TAT274. 1
12	572	94.1	129	7	Abu64232 Human FRA
13	572	94.1	129	7	Adn39126 Cancer/an
14	572	94.1	129	7	Adn39987 Cancer/an
15	572	94.1	129	8	Abm81706 Tumour-as
16	451	74.2	129	5	Aau79828 Mouse typ
17	433	71.2	309	4	Aau03500 Human TWE
18	337.5	55.5	94	7	Abu64233 Human CRY
19	274.5	45.1	112	3	Aay91463 Human sec
20	274.5	45.1	112	6	Ada57390 Human sec
21	274.5	45.1	112	7	Adc74462 Human sec
22	274.5	45.1	112	7	Add38025 Human sec
23	274.5	45.1	112	8	Adl71535 Novel hum
24	274.5	45.1	155	3	Aay91604 Human sec
25	274.5	45.1	155	6	Ada57391 Human sec

ALIGNMENTS

RESULT 1

AAW73409
ID AAW73409 standard; protein; 114 AA.

AC AAW73409;

XX 19-FEB-1999 (first entry)

XX Human secreted protein encoded by Gene No. 13.

XX Secreted protein; human; protein therapy; gene therapy; blood disorder;
pathological condition; diagnosis; cancer; neurological disorder;
developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
immune system disorder; Alzheimer's disease; cognitive disorder;
schizophrenia; prostate disease; autoimmune disorder; AIDS.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 114

XX /note= "unspecified amino acid"

XX WO9854206-A1.

XX 03-DEC-1998.

XX 28-MAY-1998; 98WO-US010868.

XX 30-MAY-1997; 97US-0044039P.

XX 30-MAY-1997; 97US-0048093P.

XX 30-MAY-1997; 97US-0048101P.

XX 30-MAY-1997; 97US-0048190P.

XX 30-MAY-1997; 97US-0048356P.

XX 30-MAY-1997; 97US-0050935P.

XX 29-AUG-1997; 97US-0056250P.

XX 29-AUG-1997; 97US-0056293P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;

XX Ni J, Peng P;

XX WPI; 1999-070209/06.

XX N-PSDB; AAV08823.

XX New isolated human genes - useful for diagnosis and treatment of, e.g.
cancers, neurological disorders, immune diseases, developmental disorders

PT or blood disorders.
 XX Claim 11; Page 153; 188pp; English.
 XX This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumors, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners
 XX Sequence 114 AA;
 SQ Query Match 100.0%; Score 608; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY .1 MARGSLRLLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 Db 1 MARGSLRLLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 QY 61 SDFCLGCAAAAPPAPRLLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114
 Db 61 SDFCLGCAAAAPPAPRLLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114
 RESULT 2
 AAW88506
 ID AAW88506 standard; protein; 129 AA.
 AC AAW88506;
 DT 30-MAR-1999 (first entry)
 XX Human liver clone HP10432-encoded membrane protein.
 XX Transmembrane protein; HP10432; human; liver.
 XX Homo sapiens.
 XX WO9855508-A2.
 XX 10-DEC-1998.
 XX 03-JUN-1998; 98WO-JP002445.
 XX 03-JUN-1997; 97JP-00144948.
 XX (SAGA) SAGAMI CHEM RES CENTRE.
 XX (PROT-) PROTEGENE INC.
 XX Kato S, Sekine S, Yamaguchi T;
 XX WPI; 1999-045730/04.
 XX N-PSDB; AAW84374.
 XX New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.
 XX Claim 1; Page 152-153; 178pp; English.

CC This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAW84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAW84359-76) coding for 18 transmembrane proteins (see AAW8491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines
 XX Sequence 129 AA;
 SQ Query Match 94.1%; Score 572; DB 2; Length 129;
 Best Local Similarity 93.9%; Pred. No. 1.6e-51;
 Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRLLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 Db 1 MARGSLRLLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 QY 61 SDFCLGCAAAAPPAPRLLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114
 Db 61 SDFCLGCAAAAPPAPRLLWPILGALSLTFVLGSLGFLVWRCRRREKFTTPI 114
 RESULT 3
 AAY57940
 ID AAY57940 standard; protein; 129 AA.
 AC AAY57940;
 XX 23-MAR-2000 (first entry)
 XX Human transmembrane protein HTMPN-64.
 XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder;
 KW reproductive disorder; smooth muscle disorder; neurological disorder;
 KW gastrointestinal disorder; developmental disorder;
 KW cell proliferative disorder.
 XX Homo sapiens.
 XX WO9961471-A2.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US011904.
 XX 29-MAY-1998; 98US-0087260P.
 XX 02-JUL-1998; 98US-0091674P.
 XX 02-OCT-1998; 98US-0102954P.
 XX 24-NOV-1998; 98US-0109869P.
 XX (INCY-) INCYTE PHARM INC.
 XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
 XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
 XX WPI; 2000-072605/06.
 XX N-PSDB; AAZ56761.
 XX Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders.
 XX Claim 1; Page 163; 229pp; English.
 XX AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human

transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN

CC Sequence 129 AA;

Query Match 94.1%; Score 572; DB 3; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLVLLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLVLLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGLLSGLFVWRRCRRRSSPPPX 114
DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGLLSGLFVWRRCRRRREKFTPI 114

RESULT 4

AAU03498
ID AAU03498 standard; protein; 129 AA.

AC AAU03498;

DT 26-SEP-2001 (first entry)

XX Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;
KW corneal graft neovascularisation; psoriasis; metastatic condition;
KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
KW preneoplastic condition; myocardial angiogenesis; wound granulation;
KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
KW peripheral atherosclerosis.

OS Homo sapiens.

Key Location/Qualifiers
FH Domain 1..78
FT /note= "Extracellular domain"
FT Peptide 1..27
FT /note= "Signal peptide"
FT Protein 28..129
FT /note= "Mature human TWEAKR protein"
FT Domain 79..101
FT /note= "Transmembrane domain"
FT Domain 102..129
FT /note= "Intracellular domain"

XX WO200145730-A2.

XX 28-JUN-2001.

XX 19-DEC-2000; 2000WO-US034755.

XX 20-DEC-1999; 99US-0172878P.

XX 10-MAY-2000; 2000US-0203347P.

XX (IMMV) IMMUNEX CORP.

XX PI

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX

DR WPI; 2001-417975/44.
XX N-PSDB; AAS03963.

XX Modulating angiogenesis in a mammal for treating diseases mediated by
PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or
PT peripheral tissue, by administering antagonist or agonist of TWEAK
XX receptor.

PS Example 1; Fig 1; 46pp; English.

XX The sequence represents the human TWEAK receptor (TWEAKR) protein. The
CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and
CC induces angiogenesis. TWEAKR may therefore be used to screen for and
CC develop TWEAKR agonists and antagonists for the modulation of
CC angiogenesis, to be used in the treatment and diagnosis of human disease.
CC The disorders mediated by angiogenesis include ocular disorders
CC characterised by ocular neovascularisation such as diabetic retinopathy,
CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,
CC retrolental fibroplasia, rubeosis, uveitis, macular degeneration and
CC corneal graft neovascularisation, and inflammatory diseases such as
CC arthritis, rheumatism and psoriasis. Other treatable diseases include
CC malignant and metastatic conditions such as sarcomas and carcinomas,
CC benign tumours and preneoplastic conditions, myocardial angiogenesis,
CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
CC plaque neovascularisation, telangiectasia, wound granulation, coronary
CC atherosclerosis, peripheral atherosclerosis and ischaemia

XX Sequence 129 AA;

Query Match 94.1%; Score 572; DB 4; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLVLLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLVLLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGLLSGLFVWRRCRRRSSPPPX 114
DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGLLSGLFVWRRCRRRREKFTPI 114

RESULT 5

ABP61512
ID ABP61512 standard; protein; 129 AA.

AC ABP61512;

DT 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 178.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW immunomodulator; cytostatic; antineoplastic; osteopathic; nootropic;
KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
XX bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-00402288.

XX 26-MAR-2001; 2001JP-0008912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX

DR WPI; 2002-583617/62.
DR N-PSDB; ABQ92000.
PT NF-approximatelykB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer.
XX
PS Claim 4; Page 814-815; 841pp; Japanese.
XX
CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition and
CC for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders
XX
SQ Sequence 129 AA;
Query Match 94.1%; Score 572; DB 5; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MARGSLRLRLVLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRAPH 60
Db 1 MARGSLRLRLVLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRAPH 60
Qy 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRREREKFTPI 114
RESULT 6
AAU79827
ID AAU79827 standard; protein; 129 AA.
XX
AC AAU79827;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human type 1 transmembrane protein Fn14.
XX
KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;
KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
KW tumour necrosis factor family; TNF family; TWEAK receptor;
KW myocardial ischaemic condition; myocardial infarction; wound healing;
KW burn healing; gastric ulcer; tissue transplantation;
KW organ transplantation; neovascularisation; vascular insufficiency;
KW cancer; inflammatory macular degeneration; diabetic retinopathy.
XX
OS Homo sapiens.
XX
PN WO200222166-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028451.
XX
PR 14-SEP-2000; 2000US-0232355P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Browning J, Burkly L, Jakubowski A, Zheng T;
XX
WPI; 2002-383103/41.
XX
PT Methods of modulating angiogenesis and inhibiting tumor progression,
PT using TWEAK receptor agonists.
XX
PS Disclosure; Fig 10A; 37pp; English.

XX
CC The invention describes methods of modulating angiogenesis and inhibiting
CC tumour progression using TWEAK (a novel member of the tumour necrosis
CC factor or TNF family) receptor agonists. Conditions which can be treated
CC using the agonists include myocardial ischaemic conditions (e.g.
CC myocardial infarction), wound healing (e.g. burn healing and healing of
CC gastric ulcers), and tissue and organ transplantations to promote
CC neovascularisation, particularly in subjects suffering from vascular
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
CC subsequently neovascularisation is useful in treatment of cancer,
CC inflammatory macular degeneration and diabetic retinopathy. This sequence
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor
CC described in the invention
XX
SQ Sequence 129 AA;
Query Match 94.1%; Score 572; DB 5; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MARGSLRLRLVLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRAPH 60
Db 1 MARGSLRLRLVLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCRRAPH 60
Qy 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRREREKFTPI 114
RESULT 7
ADA56889
ID ADA56889 standard; protein; 129 AA.
XX
AC ADA56889;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein #172.
XX
KW immunosuppressive; antiinflammatory; antiaethmatic; antiallergic;
KW cytostatic; cerebrotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
XX
DR N-PSDB; ADA55993.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX

PS Claim 13; SEQ ID NO 1079; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for

CC diagnosing, treating or preventing e.g. immune disorders, inflammatory

CC conditions, respiratory disorders, cancers, CNS disorders, or

CC neurodegenerative disorders; or polypeptides comprising an amino acid

CC sequence at least 95% identical to the new sequences. The polypeptides,

CC antibodies or antibody fragments that bind to the polypeptides, nucleic

CC acids encoding the polypeptides, agonists or antagonists that binds to

CC the polypeptide, are useful in preparing diagnostic or pharmaceutical

CC compositions for diagnosing, treating or preventing an e.g. immune

CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,

CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and

CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders

CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative

CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and

CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

CC polynucleotides are useful for chromosome identification, chromosome

CC mapping, for controlling gene expression through triple helix formation

CC or antisense DNA or RNA, in gene therapy, for identifying individuals

CC from minute biological samples, in forensic biology, and as hybridization

CC probes. The polypeptides are useful for as molecular weight markers on

CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)

CC gels, to raise antibodies, for testing biological activities, and for

CC treating or preventing neural disorders, immune system disorders,

CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,

CC renal, proliferative and/or cancerous diseases. This sequence corresponds

CC to one of the polypeptide of the invention. Note: The sequence data for

CC this patent did form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 6; Length 129;

Best Local Similarity 93.9%; Pred. No. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

DB 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFFVLGSLGFLVWRCRRRERSPPPX 114

DB 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFFVLGSLGFLVWRCRRRERSPPX 114

RESULT 8

ABUS6716

ID ABUS6716 standard; protein; 129 AA.

AC ABUS6716;

XX

XX 02-APR-2003 (first entry)

XX

DE Lung cancer-associated polypeptide #309.

XX

XX Lung cancer-associated polypeptide; cytostatic; emphysema;

XX anti-inflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;

XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX

OS Unidentified.

XX

XX WO200286443-A2.

XX

XX 31-OCT-2002.

XX

XX 18-APR-2002; 2002WO-US012476.

XX

XX 18-APR-2001; 2001US-0284770P.

XX

XX 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX

XX Aziz N, Murray R;

PI

DR WPI; 2003-093161/08.

DR N-PSDB; ABX76445.

XX

PT Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer.

XX

PS Claim 27; Page 429; 453pp; English.

XX

CC The invention relates to a method for detecting a lung cancer-associated

CC transcript in a cell from a patient, comprising contacting a biological

CC sample from the patient with a polynucleotide that selectively hybridises

CC to a sequence that is at least 80 % identical to a gene that exhibits

CC increased or decreased expression in lung cancer samples. Lung cancer-

CC associated polynucleotides and polypeptides are used for identifying a

CC compound that modulates a lung cancer-associated polypeptide, for

CC inhibiting proliferation of a lung cancer-associated cell to treat lung

CC cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful

CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,

CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful

CC for diagnostic purposes and as targets for screening for therapeutic

CC compounds that modulate lung cancer, such as antibodies. Sequences

CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the

CC invention

XX

SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 6; Length 129;

Best Local Similarity 93.9%; Pred. No. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

DB 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFFVLGSLGFLVWRCRRRERSPPPX 114

DB 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFFVLGSLGFLVWRCRRRERSPPX 114

RESULT 9

ADC74112

ID ADC74112 standard; protein; 129 AA.

XX

XX ADC74112;

AC

XX

XX 01-JAN-2004 (first entry)

DT

XX

XX Human secreted protein - SEQ ID 745.

DE

XX

XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;

XX antidiabetic; immunosuppressive; dermatological; nephrotropic;

XX antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;

XX fungicide; antiparasitic; antiarteriosclerotic; vulnary; cytostatic;

XX haemopoietic; haematologic; anaemia; autoimmune disorder;

XX rheumatoid arthritis; inflammation; Grave's disease; diabetes;

XX systemic lupus erythematosus; glomerulonephritis; neurodegenerative;

XX Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;

XX cancer; bacterial; viral; fungal; parasitic infection; gene therapy;


```
XX OS Homo sapiens.
XX PN WO2003057160-A2.
XX PD 17-JUL-2003.
XX PF 30-DEC-2002; 2002WO-US041798.
XX PR 02-JAN-2002; 2002US-0345444P.
XX PR 25-JAN-2002; 2002US-0351885P.
XX PR 25-FEB-2002; 2002US-0360068P.
XX PR 05-MAR-2002; 2002US-0362004P.
XX PR 20-MAR-2002; 2002US-0366869P.
XX PR 21-MAR-2002; 2002US-0366284P.
XX PR 28-MAR-2002; 2002US-0368679P.
XX PR 19-AUG-2002; 2002US-0404809P.
XX PR 21-AUG-2002; 2002US-0405645P.
XX PA (GETH ) GENENTECH INC.
XX PS Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;
XX PI Williams PM, Wu TD, Zhang Z;
XX PI WPI; 2003-569537/53.
XX DR N-PSDB; ADD89109.
XX PT New antibodies against tumor-associated antigenic target polypeptide,
XX PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
XX PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
XX PT carcinomas.
XX PS Claim 1; SEQ ID NO 37; 252pp; English.
XX CC The present invention relates to antibodies against tumour-associated
XX CC antigenic target polypeptide. The antibody is useful for treating or
XX CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung
XX CC cancer, breast cancer, colon cancer, ovarian cancer, prostate
XX CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The
XX CC present sequence represents a TAT polypeptide.
XX SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 7; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLSGLFVWRCRRERSPPPX 114
DB 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLSGLFVWRCRRERSPPPX 114

RESULT 12
ABU64232
ID ABU64232 standard; protein; 129 AA.
XX AC ABU64232;
XX DT 11-MAR-2004 (first entry)
XX DE Human FRADJ protein.
XX KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;
XX KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;
XX KW antiinflammatory; cardiant; ophthalmological; neuroprotective;
XX KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;
XX KW antilipemic; weight loss; obesity; diabetes.
XX OS Homo sapiens.
```

```
XX PN WO2003077939-A1.
XX PD 25-SEP-2003.
XX PF 17-MAR-2003; 2003WO-EP050066.
XX PR 19-MAR-2002; 2002US-0365851P.
XX PR 14-MAY-2002; 2002US-0380565P.
XX PA (GBST ) GENSET SA.
XX PI DiAllynas D, Lucas J, Scalia A;
XX PI WPI; 2003-779086/73.
XX DR N-PSDB; AAL56186.
XX PT Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for
XX PT treating or preventing a disorder associated with excessive weight loss
XX PT or an obesity-related disorder.
XX PS Claim 1; Page 200; 206pp; English.
XX CC The present invention provides the human FRADJ and CRYPTIC proteins.
XX CC These can be used in screening for antagonists or agonists of APMI
XX CC polypeptide or polypeptide fragment activity, comprising lipid
XX CC partitioning, lipid metabolism or insulin-like activity. The agonist or
XX CC antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for
XX CC treating or preventing a disorder associated with excessive weight loss,
XX CC comprising cachexia, cancer-related weight loss, AIDS-related weight
XX CC loss, chronic inflammatory disease-related weight loss, bulimia or
XX CC anorexia, or an obesity-related disorder, comprising obesity, insulin
XX CC resistance, atherosclerosis, atheromatous disease, heart disease,
XX CC hypertension, stroke, syndrome x, insulin or non-insulin dependent
XX CC diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related
XX CC complications, e.g., microangiopathic lesions, ocular lesions, a
XX CC retinopathy, neuropathy or renal lesions. The present sequence is a
XX CC polypeptide shown in the exemplification of the invention
XX SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 7; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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DB 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLSGLFVWRCRRERSPPPX 114
DB 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLSGLFVWRCRRERSPPPX 114

RESULT 13
ADN39126
ID ADN39126 standard; protein; 129 AA.
XX AC ADN39126;
XX DT 17-JUN-2004 (first entry)
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:444.
XX KW Human; differential expression; cancer; angiogenic disorder;
XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
XX KW inflammatory disease; autoimmune disease;
XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;
XX KW detection; diagnosis; prognosis; drug screening; drug targeting;
XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
XX KW vulnerrary; gene therapy; vaccine.
XX OS Homo sapiens.
```


CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 129 AA;
Query Match 94.1%; Score 572; DB 7; Length 129;
Best Local Similarity 93.9%; Pred. NO. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60
Db 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGLSGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGLSGFLVWRCRREREKFTTPI 114
RESULT 15
ABM81706
ID ABM81706 standard; protein; 129 AA.
XX
AC ABM81706;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO12683, SEQ:4399.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
XX
DR N-PSDB; ACN39936.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 4399; 7273pp; English.
XX
PS The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful

CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
SQ Sequence 129 AA;
Query Match 94.1%; Score 572; DB 8; Length 129;
Best Local Similarity 93.9%; Pred. NO. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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Db 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60
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Job time : 167 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 06:47:00 ; Search time 129 Seconds
(without alignments)

288.755 Million cell updates/sec

Title: US-10-062-831-59

Perfect score: 608

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Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	608	100.0	114	14	US-10-062-599-59
3	572	94.1	129	9	US-09-742-454A-4
4	572	94.1	129	9	US-09-883-777-4
5	572	94.1	129	14	US-10-044-298A-178
6	572	94.1	129	14	US-10-042-211A-178
7	572	94.1	129	15	US-10-331-496A-37
8	572	94.1	129	15	US-10-295-027-444
9	572	94.1	129	15	US-10-295-027-1305
10	572	94.1	129	15	US-10-617-217A-178
11	451	74.2	129	9	US-09-742-454A-5
12	451	74.2	129	9	US-09-883-777-5
13	433	71.2	309	9	US-09-742-454A-7

14	433	71.2	309	9	US-09-883-777-7
15	379.5	62.4	300	9	US-09-883-777-9
16	274.5	45.1	112	15	US-10-351-334-139
17	274.5	45.1	155	15	US-10-351-334-284
18	274.5	45.1	156	15	US-10-351-334-228
19	97.5	16.0	171	14	US-10-251-947-4
20	97.5	16.0	171	14	US-10-251-947-7
21	97.5	16.0	185	14	US-10-251-947-2
22	97	16.0	170	14	US-10-251-947-6
23	89.5	14.7	185	15	US-10-380-703-5
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25	89.5	14.7	1388	15	US-10-093-463-138
26	89.5	14.7	1388	15	US-10-093-463-140
27	88	14.5	184	13	US-10-087-192-984
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32	88	14.5	647	16	US-10-437-963-154909
33	87.5	14.4	186	14	US-10-251-947-14
34	87	14.3	426	15	US-10-257-174-44
35	87	14.3	426	15	US-10-343-357-6
36	85	14.0	872	16	US-10-437-963-111595
37	84	13.8	152	16	US-10-767-701-33810
38	81	13.3	484	16	US-10-437-963-162231
39	79.5	13.1	377	14	US-10-156-761-8962
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41	77	12.7	250	14	US-10-218-654-31
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ALIGNMENTS

RESULT 1

US-10-062-831-59
 ; Sequence 59, Application US/10062831
 ; GENERAL INFORMATION:
 ; APPLICANT: Steven M. Ruben, et al.
 ; TITLE OF INVENTION: 32 Human Secreted Proteins
 ; FILE REFERENCE: P2006P1
 ; CURRENT APPLICATION NUMBER: US/10/062,831
 ; PRIOR FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: 09/690,454
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US98/10868
 ; PRIOR FILING DATE: May 28, 1998
 ; PRIOR APPLICATION NUMBER: 60/044,039
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/048,093
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/048,190
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/050,935
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/048,101
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/048,356
 ; PRIOR FILING DATE: May 30, 1997
 ; PRIOR APPLICATION NUMBER: 60/056,250
 ; PRIOR FILING DATE: August 29, 1997
 ; PRIOR APPLICATION NUMBER: 60/056,296
 ; PRIOR FILING DATE: August 29, 1997
 ; PRIOR APPLICATION NUMBER: 60/056,293
 ; PRIOR FILING DATE: August 29, 1997
 ; NUMBER OF SEQ ID NOS: 229
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 59
 ; LENGTH: 114

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 Sequence 9, Appli
 Sequence 139, App
 Sequence 284, App
 Sequence 228, App
 Sequence 4, Appli
 Sequence 7, Appli
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 Sequence 6, Appli
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 Sequence 17, Appli
 Sequence 138, App
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 Sequence 33810, A
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 Sequence 8962, Ap
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 Sequence 31, Appli
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

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Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
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; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

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RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
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; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-742-454A-4

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Best Local Similarity 93.9%; Pred. No. 1.3e-46;
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Qy      61 SDFCLGCAAAAPPAPFLLWPIILGALSLLTFVLGSLGFLVWRCRRERSPPPX 114
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RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
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US-09-883-777-4

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RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
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; TYPE: PRT
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US-10-024-298A-178

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US-10-042-211A-178
; Sequence 178, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26

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; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match          94.1%; Score 572; DB 14; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1  MARGSRRLRLRLVGLWLTALLRSVAGEAQTGAPCSRSSWSADLDKCMDCASCRRPH 60
        |||||
Db      1  MARGSRRLRLRLVGLWLTALLRSVAGEAQTGAPCSRSSWSADLDKCMDCASCRRPH 60

Qy      61  SDFCLGCAAAPPPRLLWPILGGALSLTFVLGLLSGFLVRRRCRRERSPPPX 114
        |||||
Db      61  SDFCLGCAAAPPPRLLWPILGGALSLTFVLGLLSGFLVRRRCRRREKFTPI 114

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RESULT 7
US-10-331-496A-37
; Sequence 37, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 37
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-331-496A-37

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Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLRLVIGLWLLALLESVAGEAPGTPACSRGSSWSADLDKCMDCASCRAPH 60

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Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Qy 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRREKFTTPI 114

RESULT 8
US-10-295-027-444
; Sequence 444, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynné, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444.

Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRREKFTTPI 114

RESULT 9
US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NP-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
```

```
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynné, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGGLSLTFVLGLSGFLVWRRRCRRREKFTTPI 114

RESULT 10
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NP-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
```


Db 61 SDFCLGCAAAARSCDKTHTCTCPP 83
 Search completed: February 14, 2005, 06:59:18
 Job time : 130 secs

```

; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match 71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 4.7e-33;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRRAPH 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPAPFRLLPILGGALSLTFVLGLLSGFLVMRCRRERSPP 112
Db 61 SDFCLGCAAAAPAPFRLLPILGGALSLTFVLGLLSGFLVMRCRRERSPP 112

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RESULT 15
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match 62.4%; Score 379.5; DB 9; Length 300;
Best Local Similarity 88.0%; Pred. No. 5.4e-28;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRRAPH 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAA-----PPAP 74

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	608	100.0	114	4	US-09-690-454-59	Sequence 59, Appl
2	572	94.1	129	4	US-09-883-777-4	Sequence 4, Appl
3	572	94.1	129	4	US-09-949-016-6914	Sequence 6914, Ap
4	572	94.1	129	4	US-09-742-454A-4	Sequence 4, Appl
5	451	74.2	129	4	US-09-883-777-5	Sequence 5, Appl
6	451	74.2	129	4	US-09-742-454A-5	Sequence 5, Appl
7	433	71.2	309	4	US-09-883-777-7	Sequence 7, Appl
8	433	71.2	309	4	US-09-742-454A-7	Sequence 7, Appl
9	379.5	62.4	300	4	US-09-883-777-9	Sequence 9, Appl
10	274.5	45.1	112	4	US-09-489-847-139	Sequence 139, App
11	274.5	45.1	155	4	US-09-489-847-284	Sequence 284, App
12	274.5	45.1	156	4	US-09-489-847-228	Sequence 228, App
13	96.5	15.9	248	4	US-09-252-991A-29249	Sequence 29249, A
14	88.5	14.6	400	4	US-09-252-991A-26145	Sequence 26145, A
15	87.5	14.4	631	4	US-09-252-991A-20063	Sequence 20063, A
16	83.5	13.7	152	4	US-09-252-991A-31619	Sequence 31619, A
17	80.5	13.2	249	4	US-09-252-991A-29850	Sequence 29850, A
18	77	12.7	250	4	US-09-322-409-31	Sequence 31, Appl
19	77	12.7	250	4	US-09-451-527-31	Sequence 31, Appl
20	77	12.7	276	4	US-09-322-409-26	Sequence 26, Appl
21	77	12.7	276	4	US-09-451-527-26	Sequence 26, Appl
22	75	12.3	334	4	US-09-252-991A-18795	Sequence 18795, A
23	74.5	12.3	305	4	US-09-252-991A-21147	Sequence 21147, A
24	73.5	12.1	187	3	US-09-199-637A-287	Sequence 287, App
25	73.5	12.1	187	4	US-09-252-991A-21454	Sequence 21454, A
26	72.5	11.9	365	4	US-09-949-016-6907	Sequence 6907, Ap
27	72.5	11.9	391	4	US-09-949-016-7325	Sequence 7325, Ap

Qy	61	SDFCLGCAAAPPAFFLLWPILGGALSLTFVLGLISGFLVWRCRRERSPPPX	114
Dd	61	SDFCLGCAAAPPAFFLLWPILGGALSLTFVLGLISGFLVWRCRRERSPPPX	114

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RESULT 2
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

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	Query Match	94.1%	Score 572	DB 4	Length 129
	Best Local Similarity	93.9%	Pred. No. 5.1e-54		
	Matches 107	Conservative 1	Mismatches 6	Indels 0	Gaps 0
Qy	1	MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLKCMDCASCRARPH	60		
Db	1	MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLKCMDCASCRARPH	60		
Qy	61	SDFCLGCAAAPPAFRLIWPILGALSILTFVLGLSGFLVWRRCRRRSSPPX	114		
Db	61	SDFCLGCAAAPPAFRLIWPILGALSILTFVLGLSGFLVWRRCRRRKFTPI	114		

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RESULT 3
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

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Query Match	Score	DB	Length
Best Local Similarity	94.1%	572	129
Matches	93.9%	Pred. No. 5.1e-54	
Matches 107; Conservative	1;	Mismatches 6;	Indels 0;
Gaps	0;		

Qy	1	MARGSLRRLLRLVLVGLIATALLRSVAGEOAGTAPCSRGGSSWSADLDKCMDCASCRARPH	60
Db	1	MARGSLRRLLRLVLVGLIATALLRSVAGEOAGTAPCSRGGSSWSADLDKCMDCASCRARPH	60
Qy	61	SDFCLCGAAAPAPPFLRLWPIILGGALLSLTFVLGLLSGFLVMRCRRRRSSPPXP	114
Db	61	SDFCICGAAAPAPPFLRLWPIILGGALLSLTFVLGLLSGFLVMRCRRRRKFTTPI	114

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RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent NO. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

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Query Match	94.1%	Score 572;	DB 4;	Length 129;
Best Local Similarity	93.9%	Fred. No. 5.1e-54;		
Matches 107;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	MARGSLRLRLLLVLGLWLLALLRSVAGEOAPGTAPCSRGSSWSADLKCWMDCASCRRAPH	60	
Db	1	MARGSLRLRLLLVLGLWLLALLRSVAGEOAPGTAPCSRGSSWSADLKCWMDCASCRRAPH	60	
Qy	61	SDFCLGCAAAAPPAPFRLWLPIILGALSLSLTVLIGLLSGFLVWRCRRRSRPPPX	114	
Db	61	SDFCLGCAAAAPPAPFRLWLPIILGALSLSLTVLIGLLSGFLVWRCRRREKKTPI	114	

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RESULT 5
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

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Query Match	74.2%	Score 451;	DB 4;	Length 129;
Best Local Similarity	74.6%	Pred. No. 5.1e-41;		
Matches 85;	Conservative	7;	Mismatches 22;	Indels 20;

RESULT 7
 US-09-883-777-7
 ; Sequence 7, Application US/09883777
 ; Patent No. 672725
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TWEAK RECEPTOR
 ; FILE REFERENCE: 2968-C
 ; CURRENT APPLICATION NUMBER: US/09/883,777
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/172,878
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: US 60/203,347
 ; PRIOR FILING DATE: 2000-05-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/34755
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/742,454
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
 US-09-883-777-7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match      62.4%; Score 379.5; DB 4; Length 300;
Best Local Similarity 88.0%; Pred. No. 6.5e-33;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 60

Qy 61 SDFCLGCAAA-----PPAP 74
Db 61 SDFCLGCAAAARCDKTHTCPCP 83

RESULT 10
US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match      45.1%; Score 274.5; DB 4; Length 112;
Best Local Similarity 96.4%; Pred. No. 4e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 11
US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
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; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-284

Query Match      45.1%; Score 274.5; DB 4; Length 155;
Best Local Similarity 96.4%; Pred. No. 5.8e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 12
US-09-489-847-228
; Sequence 228, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-228

Query Match      45.1%; Score 274.5; DB 4; Length 156;
Best Local Similarity 96.4%; Pred. No. 5.8e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 13
US-09-252-991A-29249
; Sequence 29249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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RESULT 15
US-09-252-991A-20063
; Sequence 20063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGENOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	64	10.5	108	2	T49319	hypothetical prote
2	63	10.4	112	2	T29620	hypothetical prote
3	61	10.0	55	1	PEPE	ferredoxin 2[4Fe-4
4	61	10.0	66	2	S59086	metallothionein 3
5	61	10.0	68	2	I79866	growth inhibitory
6	61	10.0	68	2	A46034	metallothionein 3,
7	60.5	10.0	76	2	T03860	TA20 protein - com
8	59	9.7	68	2	B46034	metallothionein 3,
9	58.5	9.6	78	2	E69969	hypothetical prote
10	58	9.5	36	2	C45875	M1 class I histoc
11	58	9.5	68	2	S44391	metallothionein 3
12	57.5	9.5	92	2	T04395	probable phospholi
13	57	9.4	101	2	T26641	hypothetical prote
14	57	9.4	107	2	G72496	hypothetical prote
15	56.5	9.3	67	2	G83702	hypothetical prote
16	56.5	9.3	95	2	T06275	benzothiadiazole-i
17	56.5	9.3	109	2	E84202	ferredoxin [import
18	56	9.2	103	2	T08775	hypothetical prote
19	55.5	9.1	58	2	C69365	ferredoxin [fdx-5]
20	55.5	9.1	59	1	FEDV2N	ferredoxin 2[4Fe-4
21	55.5	9.1	85	2	H95303	hypothetical prote
22	55.5	9.1	111	2	A85866	hypothetical prote
23	55	9.0	114	2	A13204	IS66 family orf2 [
24	54	8.9	105	2	C72608	hypothetical prote
25	54	8.9	110	2	A55991	effector cell prot
26	53.5	8.8	38	2	PS0133	H-2 class I histoc
27	53.5	8.8	81	2	S39511	photosystem I iron
28	53.5	8.8	97	2	AB2120	ferredoxin [import
29	53	8.7	59	2	I51272	retinoic acid rece

A:Residues: 1-68 <PAL>
A:Cross-references: UNIPROT:P28184; GB:M93310; NID:G199133; PIDN:AAA39529.1; PID:G199134
A:Note: sequence extracted from NCBI backbone (NCBIN:108715, NCBIN:111115, NCBIP:108716)
C:Superfamily: metallothionein

Query Match 10.0%; Score 61; DB 2; Length 68;
Best Local Similarity 35.0%; Pred. No. 44;
Matches 14; Conservative 2; Mismatches 22; Indels 2; Gaps 2;

QY 31 PGTAPCSRGSSWSADLDKCMDCACRCRAPHSDFCGLGCAA 70
DB 3 PTCPCPTGSGTCS-DKC-KCKGCKCTNCKSCSCCPA 40

RESULT 7

TA20860
T3860
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03860
R:Beale, T.P.; Goldberg, R.B.
A:Submitted to the EMBL Data Library, October 1996
A:Description: Nicotiana tabacum gene expressed in anthr.
A:Reference number: Z15122
A:Accession: T03860
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-76 <BEA>
A:Cross-references: UNIPROT:O24155; EMBL:U73164; NID:G1657813; PIDN:AA18190.1; PID:G1657813
A:Experimental source: tissue-type anthr
C:Genetics:
A:Gene: TA20

Query Match 10.0%; Score 60.5; DB 2; Length 76;
Best Local Similarity 40.0%; Pred. No. 54;
Matches 12; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 40 SSWASDLKCM-----CASCRCRAPHSDFC 64
DB 27 SSVAAAGDSCTDHCAITCAFCNGKQYNYVC 56

RESULT 8

B46034
N:Alternate names: brain-specific - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B46034; S28393; JH0463; S58084; I53803
R:Palmiter, R.D.; Findley, S.D.; Whitmore, T.B.; Durnam, D.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 6333-6337, 1992
A:Title: MT-III, a brain-specific member of the metallothionein gene family.
A:Reference number: A46034; MUID:92335292; PMID:1631128
A:Accession: B46034
A:Molecule type: DNA
A:Residues: 1-68 <PAL>
A:Cross-references: UNIPROT:P25713; GB:M93311; NID:G187546; PIDN:AAA36214.1; PID:G187547
A:Note: sequence extracted from NCBI backbone (NCBIN:108717, NCBIN:111117, NCBIP:108718)
R:Tsuji, S.; Kobayashi, H.; Uchida, Y.; Ihara, Y.; Miyatake, T.
EMBO J. 11, 4843-4850, 1992
A:Title: Molecular cloning of human growth inhibitory factor cDNA and its down-regulation
A:Reference number: S28393; MUID:93099858; PMID:1464312
A:Accession: S28393
A:Molecule type: mRNA
A:Residues: 1-68 <TSU>
A:Cross-references: EMBL:D13365
R:Uchida, Y.; Takio, K.; Titani, K.; Ihara, Y.; Tomonaga, M.
Neuron 7, 337-347, 1991
A:Title: The growth inhibitory factor that is deficient in the Alzheimer's disease brain
A:Reference number: JH0463; MUID:91337462; PMID:1873033
A:Accession: JH0463
A:Molecule type: protein
A:Residues: 1-68 <UCH>

A:Note: the amino end was shown to be blocked
R:Amoureux, M.C.; Remhsaus, E.; Wurch, T.; Colpaert, F.C.; Pauwels, P.J.
submitted to the EMBL Data Library, July 1995
A:Reference number: S58084
A:Accession: S58084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-68 <AMO>
A:Cross-references: EMBL:X89604; NID:G914850; PIDN:CAA61763.1; PID:G914851
R:Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S.
Gene 144, 283-287, 1994
A:Title: Structures of the human and mouse growth inhibitory factor-encoding genes.
A:Reference number: I53803; MUID:94314230; PMID:8039715
A:Accession: I53803
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-68 <RES>
A:Cross-references: GB:S72043; NID:G565189; PIDN:AA831396.1; PID:G565190
C:Genetics:
A:Gene: GDB:MT3; GIF
A:Cross-references: GDB:I34716; OMIM:139255
A:Map position: 16q13-16q13
A:Introns: 11/1, 33/1
C:Superfamily: metallothionein
C:Keywords: Alzheimer's disease; blocked amino end; brain

Query Match 9.7%; Score 59; DB 2; Length 68;
Best Local Similarity 39.5%; Pred. No. 68;
Matches 17; Conservative 1; Mismatches 17; Indels 8; Gaps 3;

QY 31 PGTAPC-SRGSWSADLDKC--MDCASCRCRAPHSDFCGLGCAA 70
DB 3 PETCPGSGSGCTCADSCCKGCKTSCCKS-----CCSCCPA 40

RESULT 9

E69969
hypothetical protein yqzF - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69969
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertel
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
ateuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:99044033; PMID:9384377
A:Accession: E69969
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-78 <XNU>
A:Cross-references: UNIPROT:O32015; GB:Z99116; GB:AL009126; NID:G2634723; PIDN:CAB14342
A:Experimental source: strain 168
C:Genetics:
A:Gene: yqzF

Query Match 9.6%; Score 58.5; DB 2; Length 78;
Best Local Similarity 37.5%; Pred. No. 85;
Matches 15; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 74 PRLWLPILGGALSLTFVLGL--LSGFLVWRRCRRSSP 111
DB 35 PFSALW-LQGLSGFIFFAIGLYVLGAGFILYRDRKNQVSP 73

A;Map position: 4

Query Match 9.5%; Score 57.5; DB 2; Length 92;
Best Local Similarity 27.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 9; Mismatches 27; Indels 11; Gaps 2;

QY 5 S I R L R L L V I G L W L A L L R S V A G E Q A P G T A P C S R G S W S A D L D K C M D C A S C R A R P H S D F C 64
: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
D b 2 A M E R T K E L L V A M M L A L V -----V A A R A P C E V G-----Q L T V C M P A I T T G A K P S G A C C 50

QY 65 L G C A A 69
D b 51 A N L G A 55

RESULT 13
T26641
hypothetical protein Y37D8A.19 - Caenorhabditis elegans
C;Species:Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26641
R;Barlow, K.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20247
A;Accession: T26641
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-101 <WIL>
A;Cross-references: UNIPROT:O9XWU9; EMBL:AL032626; PIDN:CAA21542.1; CESP:Y37D8A.19
A;Experimental source: Clone Y37D8A
C;Genetics:
A;Gene: CESP:Y37D8A.19
A;Introns: 18/3; 34/1

Query Match 9.4%; Score 57; DB 2; Length 101;
Best Local Similarity 24.7%; Pred. No. 1.4e+02;
Matches 19; Conservative 16; Mismatches 20; Indels 22; Gaps 4;

QY 10 L R L L V L G L W L A L L R S V A G E-----Q A P G T A P C S R G S W S A D L D-----K C M D C A 53
: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
D b 1 M K L L I---V F E N I S V A A G S I I W N N N N A N R F P S C F A C S T A A G E V A N I D G S T N A R C T D A A 58

QY 54 S C R A R P H S D F C L G C A A A 70
D b 59 S N P A----E R C P G C C A S 71

RESULT 14
G72496
hypothetical protein APE2613 - Aeropyrum pernix (strain K1)
C;Species:Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72496
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; UID:99310339; PMID:10382966
A;Accession: G72496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KAW>
A;Cross-references: UNIPROT:Q9Y8I9; DDJ:AP000064; NTD:G5105945; PIDN:BAA81631.1; PID:di
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2613

Query Match 9.4%; Score 57; DB 2; Length 107;
Best Local Similarity 30.2%; Pred. No. 1.5e+02;
Matches 32; Conservative 12; Mismatches 38; Indels 24; Gaps 6;

QY 9 L I R L L V I G L W L A L L R S V A G E Q A P G T A P C S R G S W S A D L D K C M D C A S C R A R P H S D F C L G C A 68
: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :

Db 17 LKLLTASLSSATSFSAAAGMS-----SRPSSISPV--ALERSAARP-----ML 62

QY 69 AAP--PAPRLWPILGGALSTFVLGLSLGFLVWRCHRRSSPP 112
| | | | | : | | | | | : | | | | | : | | | | |

Db 63 ETPRKVGPR-LWMCFSKAWILPTILCMDRSP-----RTRASPP 100
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 15

G82702

hypothetical protein XF1281 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: G82702

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-67 <SIM>

A:Cross-references: UNIPROT:Q9PD08; GB:AE003961; GB:AE003849; NID:g9106254; PIDN:AAF8409

A:Experimental source: strain 9a5c

R:Simpsom, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuchako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1281

Query Match 9.3%; Score 56.5; DB 2; Length 67;

Best Local Similarity 33.8%; Pred. No. 1.2e+02;

Matches 22; Conservative 4; Mismatches 24; Indels 15; Gaps 4;

QY 38 RGSNSADL-DKCMDCASCARPHSDFCIG----CAAAPPPAPRLWPILGGALSLTFVL 92
| | | | | : | | | | | : | | | | | : | | | | |

Db 10 RGYSWFNDRDCSAVRSCRYGVDLDVLMSRDQCCA-----LLWLWMS---SYLMVF 59
| | | | | : | | | | | : | | | | | : | | | | |

QY 93 GLLSG 97
| | | | |

Db 60 GSGSG 64
| | | | |

Search completed: February 14, 2005, 07:13:57

Job time : 39 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	74.5	12.3	112	1	Q62B85	Q62b85 oryza sativ
2	73.5	12.1	81	2	PORD METTH	P56815 methanobact
3	67	11.0	83	2	Q8ZTF5	Q8Ztf5 pyrobaculum
4	67	11.0	90	2	Q7U455	Q7U455 synechococc
5	66	10.9	97	2	Q7NTL0	Q7ntl0 chromobacte
6	66	10.9	107	2	Q36605	Q36605 hepatitis e
7	66	10.9	107	2	Q36606	Q36606 hepatitis e
8	65	10.7	77	2	Q92MCL1	Q92mcl1 rhizobium m
9	65	10.7	105	2	Q884Q0	Q884q0 pseudomonasa
10	64.5	10.6	112	1	FLAE_MOUSE	Q9fj148 mus musculu
11	63.5	10.4	85	2	Q9P9E6	Q9P9e6 methanococc
12	63.5	10.4	85	2	Q6LX46	Q6Lx46 methanococc
13	63.5	10.4	90	2	Q6N8D2	Q6n8d2 rhodospseud
14	63	10.4	82	2	Q6ZGY2	Q6zgy2 oryza sativ
15	63	10.4	112	2	P91404	P91404 caenorhabdi
16	62.5	10.3	56	2	Q7W0S0	Q7wms0 porphyromon
17	62	10.2	54	1	FER_PEPAS	P00193 peptostrept
18	62	10.2	91	2	Q7OLU6	Q7olu6 mus musculu
19	62	10.2	98	2	Q6CCG4	Q6ccg4 yarrowia li
20	62	10.2	114	2	Q6Z6H1	Q6z6h1 oryza sativ
21	61.5	10.1	75	2	Q7OX99	Q7ox99 giardia lam
22	61.5	10.1	84	2	Q65HK2	Q65hk2 bacillus li
23	61	10.0	66	1	MT3_RAT	P27361 rattus norv
24	61	10.0	68	1	MT3_MOUSE	P28184 mus musculu
25	61	10.0	90	2	Q82PP8	Q82pp8 streptomyce
26	60.5	10.0	76	2	O24155	O24155 nicotiana t
27	60.5	10.0	89	2	Q8T258	Q8t258 methanopyru
28	60.5	10.0	101	2	Q9AX16	Q9ax16 oryza sativ
29	60	9.9	94	2	Q68VL6	Q68vl6 azoarcus sp
30	60	9.9	100	2	Q7VBB2	Q7vbb2 prochloroco
31	59.5	9.8	58	2	Q68GX9	Q68gx9 canis lupus

```
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL J. Bacteriol. 179:7135-7155(1997).
CC -|- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -|- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
CC -|- CAUTION: There seems to be a sequencing error that fuses together
CC porc and pord. We have cut the ORF into its two constituents.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000929; AAB86210.1; ALT_INIT.
CC HSPF; P00195; 1CLF.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC Pfam; PF00037; Fer4; 2.
CC PRINTS; PR00353; 4FE4S_FERREDOXIN.
CC PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
CC 4Fe-4S; Complete proteome; Electron transport; Iron-sulfur;
CC Oxidoreductase; Repeat.
CC METAL 34 34 Iron-sulfur 1 (4Fe-4S) (Potential).
CC METAL 37 37 Iron-sulfur 1 (4Fe-4S) (Potential).
CC METAL 40 40 Iron-sulfur 1 (4Fe-4S) (Potential).
CC METAL 44 44 Iron-sulfur 2 (4Fe-4S) (Potential).
CC METAL 60 60 Iron-sulfur 2 (4Fe-4S) (Potential).
CC METAL 63 63 Iron-sulfur 2 (4Fe-4S) (Potential).
CC METAL 66 66 Iron-sulfur 2 (4Fe-4S) (Potential).
CC METAL 70 70 Iron-sulfur 1 (4Fe-4S) (Potential).
CC SEQUENCE 81 AA; 9121 MW; 219A9CCAE8A41604 CRC64;
CC -----
CC Query Match 12.1%; Score 73.5; DB 1; Length 81;
CC Best Local Similarity 29.2%; Pred. No. 16;
CC Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;
CC -----
CC 31 PGTAFCPSRGSGWSA-----DLDKMDCASCRA-----RPHS---DFCLGCA-AAPPA 73
CC 11 PGSTVKNKTGWRTPKPVLDKDKICDCNCLFCPEGCINREHEIDYDYCKGCGICAEKC 70
CC -----
CC 74 PPRLL 78
CC 71 PVKAI 75
CC -----
CC Query Match 11.0%; Score 67; DB 2; Length 90;
CC Best Local Similarity 27.8%; Pred. No. 71;
CC Matches 30; Conservative 12; Mismatches 32; Indels 34; Gaps 4;
CC -----
CC 7 RRLRLVLVLGLMALLRSVAGEQAPGTAPCSRSGSWADLDKCMDCASCRAPHSHDFCLG 66
CC 11 RRLRLVLVLGLMALLRSVAGEQAPGTAPCSRSGSWADLDKCMDCASCRAPHSHDFCLG 66
CC -----
CC 67 CAAPAPPFRLW-PILGGALSLTFVLGLSLGFLVW---RRCRRERS 110
CC 49 -----FOALWQPLFTPAISLLIMALLSGILSWQRRVLKTRDS 88
CC -----
CC RESULT 5
CC Q7NTL0 PRELIMINARY; PRT; 97 AA.
CC ID Q7NTL0
CC AC Q7NTL0;
CC DT 01-MAR-2004 (TrEMBLrel. 26, Created)
CC DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
CC DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CC DE Hypothetical protein.
CC GN OrderedLocustNames=CV3044;
CC OS Chromobacterium violaceum.
CC OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
```

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RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RL aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009922; AAL64806.1; -.
DR HSPF; P00193; 1DUR.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4S_FERREDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
CC 4Fe-4S; Complete proteome; Iron-sulfur; Metal-binding.
CC SEQUENCE 83 AA; 8999 MW; 11EE9466C4807A37 CRC64;
CC -----
CC Query Match 11.0%; Score 67; DB 2; Length 83;
CC Best Local Similarity 30.4%; Pred. No. 66;
CC Matches 17; Conservative 4; Mismatches 13; Indels 22; Gaps 3;
CC -----
CC 34 APCSRG--SSWS-----ADLDKCMDCASC-----RAPHSDPFLG 67
CC 8 APASAGITGIRTYKYPVNLKSCIDCGLCWLVCPSVIDWEKGTIKVIDYDFCKGC 63
CC -----
CC RESULT 4
CC Q7U455 PRELIMINARY; PRT; 90 AA.
CC ID Q7U455
CC AC Q7U455;
CC DT 01-OCT-2003 (TrEMBLrel. 25, Created)
CC DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
CC DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CC DE Hypothetical protein precursor.
CC GN OrderedLocustNames=SYNW2217;
CC OS Synecococcus sp. (strain WH8102).
CC OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
CC OX NCBI_TaxID=84588;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
CC RA Palenik B., Brahmsha B., Larimer F.W., Land M.L., Hauser L.,
CC Chain P., Lamerdin J.E., Regalia W., Allen E.E., McCarren J.,
CC Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
CC "The genome of a motile marine Synecococcus.";
CC RL Nature 424:1037-1042(2003).
CC DR EMBL; BX569695; CA808732.1; -.
CC KW Complete proteome; Hypothetical protein; Signal.
CC FT SIGNAL 1 37 Potential.
CC SEQUENCE 90 AA; 10051 MW; 82FAA501C7C64958 CRC64;
CC -----
CC Query Match 11.0%; Score 67; DB 2; Length 90;
CC Best Local Similarity 27.8%; Pred. No. 71;
CC Matches 30; Conservative 12; Mismatches 32; Indels 34; Gaps 4;
CC -----
CC 7 RRLRLVLVLGLMALLRSVAGEQAPGTAPCSRSGSWADLDKCMDCASCRAPHSHDFCLG 66
CC 11 RRLRLVLVLGLMALLRSVAGEQAPGTAPCSRSGSWADLDKCMDCASCRAPHSHDFCLG 66
CC -----
CC 67 CAAPAPPFRLW-PILGGALSLTFVLGLSLGFLVW---RRCRRERS 110
CC 49 -----FOALWQPLFTPAISLLIMALLSGILSWQRRVLKTRDS 88
CC -----
CC RESULT 5
CC Q7NTL0 PRELIMINARY; PRT; 97 AA.
CC ID Q7NTL0
CC AC Q7NTL0;
CC DT 01-MAR-2004 (TrEMBLrel. 26, Created)
CC DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
CC DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CC DE Hypothetical protein.
CC GN OrderedLocustNames=CV3044;
CC OS Chromobacterium violaceum.
CC OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22828280; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Axaripa J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carriazo D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chusere L.M.O.,
RA Crezyanski-Paea T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R., Ferro J.A.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Griebard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyza M.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento P.F., Nicolas M.P., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seauanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL; AE016920; AAQ60713.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 97 AA; 10929 MW; FALEFEFB8B7DB7D CRC64;

Query Match 10.9%; Score 66; DB 2; Length 97;
Best Local Similarity 25.2%; Pred. No. 95;
Matches 29; Conservative 12; Mismatches 34; Indels 40; Gaps 3;

QY 6 LRLRLVGLVWLALLRSVAGEQAPGTAPCSRGSWSADLDKMDKMDCSRPHSDFCL 65
Db :||||:||||:
1 MRYLLRIVELALLLVAVTVQNSHVEPKLFFGQSWs----- 38

QY 66 GCAAPPAPFRLWILGALSLTFLVGLLSGLFVWRRCRE-----RSSPP 112
Db ||||:||||:
39 ----APFIVFLLLFFVVGAA-----VGLLATFSYKTRRLSOLKXELNRPP 83

RESULT 6
ID O36605 PRELIMINARY; PRT; 107 AA.
AC O36605;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Strain Morocco/F23 ORF-1 (Fragment).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Morocco/F23;
RX MEDLINE=97475412; PubMed=9334924;
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMV53.3.CO;2-O;
RA Chatterjee R., Tearev S., Pillot J., Coursaget P., Emerson S.U.,
RA Purcell R.H.;
RT "African strains of hepatitis E virus that are distinct from Asian
RT strains.";
RL J. Med. Virol. 53:139-144(1997).
DR EMBL; AF010429; AAB66553.1; -.
DT InterPro; IPR009080; trnasyn_la_bind.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 10934 MW; 7F60EDCE2E567F8 CRC64;

Query Match 10.9%; Score 66; DB 2; Length 107;
Best Local Similarity 27.2%; Pred. No. 1e+02;
Matches 25; Conservative 8; Mismatches 27; Indels 32; Gaps 4;

QY 35 PCSRGSSWSADLDKC-----MDCASCRARPHSDFCIGCAAAAPPAPFRLWLPIL 82
Db ||||:||||:
20 PFSPGHVWESANPFGESTLTYRTWSEVDAASNAQPD-----LGLASEPPIPSRAATPIL 75

QY 83 GGALSLTFLVGLLSGLFVWRRCRRERSPPPX 114
Db ||||:
76 AAPLP-----SIVPG-----PTPPPS 91

RESULT 7
ID O36606 PRELIMINARY; PRT; 107 AA.
AC O36606;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Strain Morocco/F12 ORF-1 (Fragment).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Morocco/F12;
RX MEDLINE=97475412; PubMed=9334924;
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMV53.3.CO;2-O;
RA Chatterjee R., Tearev S., Pillot J., Coursaget P., Emerson S.U.,
RA Purcell R.H.;
RT "African strains of hepatitis E virus that are distinct from Asian
RT strains.";
RL J. Med. Virol. 53:139-144(1997).
DR EMBL; AF010429; AAB66553.1; -.
DT InterPro; IPR009080; trnasyn_la_bind.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 10934 MW; 7F60EDCE2E567F8 CRC64;

Query Match 10.9%; Score 66; DB 2; Length 107;
Best Local Similarity 27.2%; Pred. No. 1e+02;
Matches 25; Conservative 8; Mismatches 27; Indels 32; Gaps 4;

QY 35 PCSRGSSWSADLDKC-----MDCASCRARPHSDFCIGCAAAAPPAPFRLWLPIL 82
Db ||||:||||:
20 PFSPGHVWESANPFGESTLTYRTWSEVDAASNAQPD-----LGLASEPPIPSRAATPIL 75

QY 83 GGALSLTFLVGLLSGLFVWRRCRRERSPPPX 114
Db ||||:
76 AAPLP-----SIVPG-----PTPPPS 91

RESULT 8
ID O92MCI PRELIMINARY; PRT; 77 AA.
AC O92MCI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE HYPOTHETICAL TRANSMEMBRANE PROTEIN.
OS ORFNames=SMC00666;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
```

OX NCBI_TaxID=1076;
RN [1] -
RP SEQUENCE FROM N.A.

DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Oxidoreducta

RC STRAIN-CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.,
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospirillum rubrum.",
RL Nat. Biotechnol. 22:55-61 (2004).
DR EMBL; BX572599; CAE27412.1; -.
DR InterPro; IPR010710; DUF1289.
DR Pfam; PF06945; DUF1289; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 90 AA; 9748 MW; F75820762545F607 CRC64;

Query Match 10.4%; Score 63.5; DB 2; Length 90;
Best Local Similarity 30.2%; Pred. No. 1.5e+02;
Matches 19; Conservative 6; Mismatches 33; Indels 5; Gaps 3;

QY 32 GTPACRSGSSWADLDKMDKDCASCRPHSDFCIGCAAPAPPELLWPIILGGALSLTFV 91
Db 7 GDQCQPPSDMSIE-TPCI--AVCMINPQTNLCYCGRTMPEIAR--WPRMDSAERLAIM 61

QY 92 LGL 94
Db 62 AGL 64

RESULT 14
Q6ZGV2 PRELIMINARY; PRT; 82 AA.
AC Q6ZGV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein QJ1743_B12.31.
GN Name=QJ1743_B12.31;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004096; BAD07679.1; -.
KW Hypothetical protein.
SQ SEQUENCE 82 AA; 8828 MW; 2675B6BB26CF52F3 CRC64;

Query Match 10.4%; Score 63; DB 2; Length 82;
Best Local Similarity 29.5%; Pred. No. 1.6e+02;
Matches 28; Conservative 5; Mismatches 20; Indels 42; Gaps 5;

QY 30 AFGTAP-----CS-----RGSGWSADLDKMDKDCASCRPHSDFCIGCAAPAPPELLW 79
Db 7 SPSTTFAAACSCSLSPWTRCSSWS-----LGCATS-----RRSL 40

QY 80 PILGGALSLTFVLGLLSGLVWRRCRRSSPPXP 114
Db 41 PCLCTSLRATPLPL-----HRPCRLHRCPPPR 69

RESULT 15
P91404 PRELIMINARY; PRT; 112 AA.
ID P91404;
AC P91404;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein R10A10.2.
GN Name=R10A10.2; ORFNames=R10A10.2;
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.",
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX Wansley P., Bradshaw H.;
RT "The sequence of C. elegans cosmid R10A10.",
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; U80449; AAB37826.1; -.
DR PIR; T29620; T29620.
DR HSSP; P28990; 1CHC.
DR WormBase; WEGene00019993; R10A10.2.
DR WormPep; R10A10.2; CE12670.
DR GO; GO:0000151; C-ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F-ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR GO; GO:0016567; P-protein ubiquitination; IEA.
DR InterPro; IPR001841; ZnfRING.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00983; LX6 UPAR; UNKNOWN_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 112 AA; 12871 MW; 8F797E10FB701092 CRC64;

Query Match 10.4%; Score 63; DB 2; Length 112;
Best Local Similarity 27.5%; Pred. No. 2.1e+02;
Matches 19; Conservative 8; Mismatches 22; Indels 20; Gaps 3;

QY 11 RLLVLGLWLLRLRSVAGEQAFGTAPCRSGWSADLDKMDKDCASCRPHSDFCIGCAA 70
Db 28 RPFVLKKWNL-----AVWAWDVE-CDTCAICRVHLMEE-CLRCQSE 67

QY 71 PPAPPELLW 79
Db 68 PSAECYVVM 76

Search completed: February 14, 2005, 07:13:14
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:47:40 ; Search time 163 Seconds
(without alignments)
270.495 Million cell updates/sec

Title: US-10-062-831-59
Perfect score: 608
Sequence: 1 MARGSLRLRLVGLWLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1221546

Minimum DB seq length: 0
Maximum DB seq length: 114

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980a:*
- 2: Geneseqp1990a:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001a:*
- 5: Geneseqp2002a:*
- 6: Geneseqp2003a:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608	100.0	114	2	AAW73409 Human sec
2	337.5	55.5	94	7	ABU64233 Human CRY
3	274.5	45.1	112	3	AA91463 Human sec
4	274.5	45.1	112	6	ADA57390 Human sec
5	274.5	45.1	112	7	ADC74462 Human sec
6	274.5	45.1	112	7	ADD38025 Human sec
7	274.5	45.1	112	8	ADL71535 Novel hum
8	191	31.4	32	6	ADA49370 Human Fnl
9	73.5	12.1	98	6	AAU66196 Propionib
10	73.5	12.1	98	6	ABM62715 Propionib
11	70	11.5	70	5	AAE22260 Human BAF
12	69	11.3	79	5	ABP06392 Human ORF
13	68.5	11.3	101	2	AA74100 Human pro
14	68.5	11.3	114	4	AAU57190 Propionib
15	68.5	11.3	114	6	ABM53709 Propionib
16	68	11.2	70	5	AAE22254 Human BAF
17	68	11.2	70	5	AAE22263 Human BAF
18	68	11.2	112	7	ABO72961 Pseudomon
19	67.5	11.1	74	4	AAU47590 Propionib
20	67.5	11.1	74	6	ABM44109 Propionib
21	67	11.0	70	5	AAE22259 Human BAF
22	67	11.0	74	2	AA31398 HEV pepti
23	67	11.0	111	4	AAU42650 Propionib
24	67	11.0	111	6	ABM39169 Propionib
25	66	10.9	70	5	AAE22261 Human BAF

26	66	10.9	70	5	AAE22252 Human BAF
27	65	10.7	70	5	AAE22255 Human BAF
28	65	10.7	70	5	AAE22257 Human BAF
29	65	10.7	70	5	AAE22265 Human BAF
30	65	10.7	70	5	AAE22264 Human BAF
31	65	10.7	87	8	ABO54761 Human gen
32	65	10.7	92	8	ADP29374 Human sec
33	64.5	10.6	61	4	AAU53825 Propionib
34	64.5	10.6	61	6	ABM50344 Propionib
35	64.5	10.6	112	8	ADJ76375 Marker ge
36	64.5	10.6	112	8	ADN43102 Amino aci
37	64.5	10.6	112	8	ADP74023 Murine on
38	64	10.5	65	8	ABO57703 Human gen
39	64	10.5	77	2	AA12612 Human 5'
40	64	10.5	95	7	ABO67894 Pseudomon
41	64	10.5	100	4	AAE04262 Human gen
42	63.5	10.4	78	4	AAU58568 Propionib
43	63.5	10.4	78	6	ABM55087 Propionib
44	63	10.4	70	5	AAE22253 Human BAF
45	63	10.4	70	5	AAE22262 Human BAF

ALIGNMENTS

RESULT 1
AAW73409
ID AAW73409 standard; protein; 114 AA.
XX
AC AAW73409;
XX
DT 19-FEB-1999 (first entry)
XX
DE Human secreted protein encoded by Gene No. 13.
XX
KW Secreted protein; human; protein therapy; gene therapy; blood disorder;
KW pathological condition; diagnosis; cancer; neurological disorder;
KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
KW immune system disorder; Alzheimer's disease; cognitive disorder;
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 114
FT /note= "unspecified amino acid"
XX
PN WO9854206-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-US010868.
XX
PR 30-MAY-1997; 97US-0044039P.
PR 30-MAY-1997; 97US-0048093P.
PR 30-MAY-1997; 97US-0048101P.
PR 30-MAY-1997; 97US-0048190P.
PR 30-MAY-1997; 97US-0048356P.
PR 30-MAY-1997; 97US-0050935P.
PR 29-AUG-1997; 97US-0056250P.
PR 29-AUG-1997; 97US-0056293P.
PR 29-AUG-1997; 97US-0056296P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;
PI Ni J, Feng P;
XX
DR WPI; 1999-070209/06.
DR N-PSDB; AAV08823.
XX
PT New isolated human genes - useful for diagnosis and treatment of, e.g.
PT cancers, neurological disorders, immune diseases, developmental disorders

PT or blood disorders.
XX Claim 11; Page 153; 189pp; English.
XX
XX This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners
XX
SQ Sequence 114 AA;
Query Match 100.0%; Score 608; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.6e-55; Mismatches 0; Indels 0; Gaps 0;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Qy 61 SDFCLGCAAPAPPRLLWLPILGGALSLTFVLGLSGFLVWRCRRERSPPPX 114
Db 61 SDFCLGCAAPAPPRLLWLPILGGALSLTFVLGLSGFLVWRCRRERSPPPX 114
RESULT 2
ABU64233 ID ABU64233 standard; protein; 94 AA.
XX AC ABU64233;
XX DT 11-MAR-2004 (first entry)
XX DE Human CRYPTIC protein.
XX KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist; antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV; antiinflammatory; cardiant; ophthalmological; neuroprotective; nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive; antilipemic; weight loss; obesity; diabetes.
XX OS Homo sapiens.
XX PN WO2003077939-A1.
XX PD 25-SEP-2003.
XX PF 17-MAR-2003; 2003WO-EP050066.
XX PR 19-MAR-2002; 2002US-0365851P.
XX PR 14-MAY-2002; 2002US-0380565P.
XX PA (GEST) GENSET SA.
XX PI Dialynas D, Lucas J, Scalia A;
XX WPI; 2003-779086/73.
XX DR N-PSDB; AAL56187.
XX PT Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for treating or preventing a disorder associated with excessive weight loss

PT or an obesity-related disorder.
XX Claim 2; Page 201; 206pp; English.
XX
XX The present invention provides the human FRADJ and CRYPTIC proteins. These can be used in screening for antagonists or agonists of APM1 polypeptide or polypeptide fragment activity, comprising lipid partitioning, lipid metabolism or insulin-like activity. The agonist or antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for treating or preventing a disorder associated with excessive weight loss, comprising cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease-related weight loss, bulimia or anorexia, or an obesity-related disorder, comprising obesity, insulin resistance, atherosclerosis, atheromatous disease, heart disease, hypertension, stroke, syndrome X, insulin or non-insulin dependent diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related complications, e.g., microangiopathic lesions, ocular lesions, retinopathy, neuropathy or renal lesions. The present sequence is a polypeptide shown in the exemplification of the invention
XX
SQ Sequence 94 AA;
Query Match 55.5%; Score 337.5; DB 7; Length 94;
Best Local Similarity 63.2%; Pred. No. 2.9e-27; Mismatches 72; Conservative 1; Mismatches 6; Indels 35; Gaps 1;
Qy 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Qy 61 SDFCLGCAAPAPPRLLWLPILGGALSLTFVLGLSGFLVWRCRRERSPPPX 114
Db 33 -----AAPPAPPRLLWLPILGGALSLTFVLGLSGFLVWRCRRREKFTPI 79
RESULT 3
AA91463 ID AA91463 standard; protein; 112 AA.
XX AC AA91463;
XX DT 29-JUN-2000 (first entry)
XX DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
XX KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.
XX OS Homo sapiens.
XX PN WO200006698-A1.
XX PD 10-FEB-2000.
XX PF 29-JUL-1999; 99WO-US017130.
XX PR 30-JUL-1998; 98US-0094657P.
XX PR 05-AUG-1998; 98US-0095486P.
XX PR 06-AUG-1998; 98US-0095454P.
XX PR 06-AUG-1998; 98US-0095455P.
XX PR 12-AUG-1998; 98US-0096319P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX WPI; 2000-195282/17.
XX DR N-PSDB; AAA26358.

XX New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 11; Page 45; 634pp; English.
XX
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91491. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; neurotropic; neuroprotective;
CC antiallergic; osteoprotective; antiarthritic; antibacterial; antidiabetic;
CC antiasthma; antipeptic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 112 AA;
XX
XX Query Match 45.1%; Score 274.5; DB 3; Length 112;
XX Best Local Similarity 96.4%; Pred. No. 1.2e-20;
XX Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
OY 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTPACSRGSSWSADLDKMDCA-SC 55
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTPACSRGSSWSADLDKMDCTSC 56
RESULT 4
ADA57390
ID ADA57390 standard; protein; 112 AA.
XX
XX ADA57390;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted protein #172.
XX
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
XX cytostatic; cerebroprotective; neuroprotective; neurotropic;
XX cardiovascular; antiarteriosclerotic; gene therapy;
XX human secreted protein; immune disorder; inflammation;
XX respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
XX inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
XX multiple sclerosis; ischaemic brain injury; Parkinson's disease;
XX Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
XX triple helix formation; antisense gene therapy; forensic biology.
XX
XX Homo sapiens.
XX
XX WO2002102994-A2.
XX
XX 27-DEC-2002.
XX
XX 19-MAR-2002; 2002WO-US008278.
XX
XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2003-167512/16.
XX N-PSDB; ADA56496.
XX
XX New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders.
XX
XX Claim 13; SEQ ID NO 1582; 1754pp; English.
XX
XX The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome
XX mapping, for controlling gene expression through triple helix formation
XX or antisense DNA or RNA, in gene therapy, for identifying individuals
XX from minute biological samples, in forensic biology, and as hybridization
XX probes. The polypeptides are useful for as molecular weight markers on
XX sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
XX gels, to raise antibodies, for testing biological activities, and for
XX treating or preventing neural disorders, immune system disorders,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal, proliferative and/or cancerous diseases. This sequence corresponds
XX to one of the polypeptide of the invention. Note: The sequence data for
XX this patent did form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 112 AA;
XX
XX Query Match 45.1%; Score 274.5; DB 6; Length 112;
XX Best Local Similarity 96.4%; Pred. No. 1.2e-20;
XX Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
OY 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTPACSRGSSWSADLDKMDCA-SC 55
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTPACSRGSSWSADLDKMDCTSC 56
RESULT 5
ADC74462
ID ADC74462 standard; protein; 112 AA.
XX
XX ADC74462;
XX
XX ADC74462;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human secreted protein - SEQ ID 1095.
XX
XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
XX antidiabetic; immunosuppressive; dermatological; nephrotropic;
XX antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;
XX fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
XX haemopoietic; haematologic; anaemia; autoimmune disorder;

KW hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW respiratory disorder; pulmonary disorder; connective tissue disorder;
KW skin disorder; CNS disorder; congenital disorder; infectious disorder;
KW gastrointestinal disorder; human; secreted protein.
XX
OS Homo sapiens.
XX
XX US2004034196-A1.
XX
XX 19-FEB-2004.
XX
XX 27-JAN-2003; 2003US-00351334.
XX
XX 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096313P.
PR 29-JUL-1999; 99WO-US017130.
PR 24-JAN-2000; 2000US-00498847.
PR 25-JAN-2002; 2002US-0350898P.
XX
XX (KOMA/) KOMATSOUIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHI/) SHI Y.
PA (LAFL/) LAFLUR D W.
PA (WEI/) WEI Y.
XX
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan DR, Moore PA, Shi Y;
PI Lafleur DW, Wei Y;
PI
XX WPI; 2004-180094/17.
DR N-PSDB; ADL71419.
XX
XX New human secreted nucleic acid, useful for diagnosing and treating
PT neurodegenerative, inflammatory, hyperproliferative, metabolic,
PT reproductive, cardiovascular, respiratory or immunological disorders or
PT diseases.
XX
PS Claim 11; SEQ ID NO 139; 234pp; English.
XX
XX The invention describes an isolated human nucleic acid molecule (I)
CC comprising a polynucleotide having a nucleotide sequence at least 95%
CC identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
CC the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
CC to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
CC epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
CC sequence included in ATCC deposit No: Z, which is hybridisable to SEQ ID
CC NO: X, having a biological activity. The nucleic acids and polypeptides,
CC pharmaceutical formulations and kits are useful in diagnosing and
CC treating neurodegenerative diseases states, behavioral disorders,
CC inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
CC disease, Parkinson's disease or Huntington's disease), metabolic
CC disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
CC disorders, immunological disorders (e.g. arthritis, asthma or AIDS),
CC endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
CC or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
CC cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
CC conditions afflicting connective tissue, skin disorders, CNS disorders,
CC congenital disorders, infectious disorders and gastrointestinal
CC disorders. This is the amino acid sequence of a novel human secreted
CC protein of the invention. Note: This sequence does not appear in the US
CC printed specification but is available in electronic format from the US
CC patent office at ftp.seqdata.uspto.gov/seqdata.html?DocID=20040034196.
XX

SQ Sequence 112 AA;
Query Match 45.1%; Score 274.5; DB 8; Length 112;
Best Local Similarity 96.4%; Pred. No. 1.2e-20;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MARGSLRELLRLVLGLMALLRSVAGQAPGCTAPCSRGSWSADLDKMDCA-SC 55
DB 1 MARGSLRELLRLVLGLMALLRSVAGQAPGCTAPCSRGSWSADLDKMDCTSC 56
RESULT 8
ADA49370
ID ADA49370 standard; peptide; 32 AA.
XX
XX ADA49370;
XX 20-NOV-2003 (first entry)
XX Human Fn14 cysteine rich domain.
XX
XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
XX antiarthritic; dermatological; antidiabetic; neuroprotective;
XX antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX insulin dependent diabetes mellitus; multiple sclerosis;
XX myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
XX autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
XX pemphigus vulgaris; acute rheumatic fever;
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; Fn14; CRD;
XX cysteine rich domain.
XX
XX Homo sapiens.
XX WO2003035846-A2.
XX
XX 01-MAY-2003.
XX
XX 24-OCT-2002; 2002WO-US034376.
XX
XX 24-OCT-2001; 2001US-0345106P.
PR 14-JAN-2002; 2002US-0348962P.
PR 07-FEB-2002; 2002US-0354966P.
PR 13-AUG-2002; 2002US-0403364P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Zhang G, Shu H, Liu Y, Xu L;
XX WPI; 2003-403345/38.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.
XX
PS Disclosure; Page 618; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting abgt; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and

```
CC polyarthritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human Fn14.
XX
SQ Sequence 32 AA;

Query Match 31.4%; Score 191; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CSRSSWSADLDKCMDCASCRARPHSDFLGCG 67
DB 1 CSRSSWSADLDKCMDCASCRARPHSDFLGCG 32

RESULT 9
AAU66196
ID AAU66196 standard; protein; 98 AA.
XX
AC AAU66196;
XX
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #27092.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59719.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 27391; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
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CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 98 AA;

Query Match 12.1%; Score 73.5; DB 4; Length 98;
Best Local Similarity 30.3%; Pred. No. 8.7;
Matches 33; Conservative 9; Mismatches 34; Indels 33; Gaps 8;

QY 18 WLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPHSDFLGCGA-----AA 70
DB 2 WSSLVESV-----PRATIC--GEEMHSGGDVVF---RVRRPVSTGVPGCAPRCRCWAR 51
QY 71 PP---APFRLLPFI-----LGALS-LTFVLGLSGFLVRRRCR 105
DB 52 QPLVCSFWDRFVPVRSFGRSRSLSMGTSGGTRAMGLPAP--SWRRRCR 98

RESULT 10
ABM62715
ID ABM62715 standard; protein; 98 AA.
XX
AC ABM62715;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #27391.
XX
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallieve-Douglas J;
XX
XX WPI; 2003-381789/36.
XX
XX N-PSDB; ACF64648.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
XX
XX Example 1; SEQ ID NO 27391; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention
XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes
XX polypeptide and an isolated T cell population comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or
XX antigen-presenting cells that express the polypeptide; a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a
XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne
```

CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 98 AA;

Query Match 12.1%; Score 73.5; DB 6; Length 98;
Best Local Similarity 30.3%; Pred. No. 8.7;
Matches 33; Conservative 9; Mismatches 34; Indels 33; Gaps 8;
QY 18 WLALRSVAGQAPGTATPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA-----AA 70
DB 2 WSSLVESV-----PRATIC--GEWHSGGDVVF---RVRARPVSTGVGCAFWCRCSWAR 51
QY 71 PP---APPRLWPI-----LGGALS-LTFVLGLSGFLVWRRCR 105
DB 52 QPLVCSPWDRFPVWRSPGRRSLSMGGTSGGTRAWGLPAP--SWRRCR 98

RESULT 11
ID AAE22260 standard; protein; 70 AA.
XX
AC AAE22260;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human BAFF-R:Fc clone fusion protein, JST678.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW IGG; immunoglobulin G; fusion protein.
XX
OS Homo sapiens.
XX
FN WO200224909-A2.
XX
PD 28-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US028006.
XX
PR 18-SEP-2000; 2000US-0233152P.
PR 21-SEP-2000; 2000US-0234140P.
PR 13-FEB-2001; 2001US-0268499P.
PR 14-AUG-2001; 2001US-0312185P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Ambrose CW, Thompson JS;
XX
DR WPI; 2002-362428/39.
XX
PT New human BAFF receptor proteins and nucleic acids, useful for treating,
PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
PT genetic disorders involving B-cells, cardiovascular disorders, or renal
PT disorders.
XX
PS Claim 44; Fig 20; 164pp; English.
XX
CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour

CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hyperension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BBFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present protein sequence is human BAFF-R:immunoglobulin G Fc region
CC clone fusion protein
XX
XX Sequence 70 AA;

Query Match 11.5%; Score 70; DB 5; Length 70;
Best Local Similarity 32.2%; Pred. No. 14;
Matches 19; Conservative 6; Mismatches 28; Indels 6; Gaps 2;

QY 23 RSVAGEQAPGTAPCSRSSWSADLDKCMDCASCRARPHSDFCLGCAAPAPFPRLWLP 80
DB 5 RSLGRDAPAPTFCNPAECFDALVRHCGLLRPKP-----AGASSPAPRTALQP 58

RESULT 12
ID ABP06392 standard; protein; 79 AA.
XX
AC ABP06392;
XX
DT 25-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:12766.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
FN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
XX
DR N-PSDB; ABN22144.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,


```
PT hyperproliferative disorders and autoimmune disorders.
XX
XX Disclosure, SEQ ID NO 12766; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 79 AA;
XX
XX Query Match 11.3%; Score 69; DB 5; Length 79;
XX Best Local Similarity 26.0%; Pred. No. 20;
XX Matches 19; Conservative 14; Mismatches 28; Indels 12; Gaps 4;
XX
Qy 4 GSLRRLRLVGLVGLLALLRSVAGEQ-----APGTAPCGSGSSW-SADLDKMDCAS 54
Db 7 GLLHFRFRLAIGLLLAIEVLAKRGKCPNKPSCPSKPCCSADGYCGGAEQC--TSG 64
XX
Qy 55 CRARPHSDFCLGC 67
Db 65 CQPQ-YSQYPPSC 76
XX
RESULT 13
AAU74100
ID AAU74100 standard; protein; 101 AA.
XX
XX AAU74100;
XX
XX 14-MAR-2000 (first entry)
XX
XX Human prostate tumor EST fragment derived protein #287.
XX
XX Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
XX treatment.
XX
XX Homo sapiens.
XX
XX DE19820190-A1.
XX
XX 04-NOV-1999.
XX
XX 28-APR-1998; 98DE-01020190.
XX
XX 28-APR-1998; 98DE-01020190.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX WPI; 1999-621386/54.
XX
XX N-PSDB; AA252952.
XX
XX
XX New human nucleic acid sequences from pancreatic tumors, and related
XX proteins.
XX
XX Claim 23; Page 428; 502pp; German.
XX
XX This invention describes novel polypeptides and their encoding nucleic
XX acids derived from human pancreatic tumor tissue which have cytostatic
XX activity. The sequences are also useful in producing pharmaceutical
XX compositions for treatment of pancreatic tumors. AAY73814-Y74252
XX represent protein fragments encoded by the human pancreatic tumor cDNA
XX library derived expressed sequence tag (EST) sequences represented in
XX AA252858-Z53014
XX
XX Sequence 101 AA;
XX
XX Query Match 11.3%; Score 68.5; DB 2; Length 101;
XX Best Local Similarity 26.0%; Pred. No. 30;
XX Matches 25; Conservative 12; Mismatches 26; Indels 33; Gaps 5;
XX
Qy 16 GLWLALLRSVAGEQAPGTAPCGSGSSW-SADLDKMDCASCRARPHSDFCLG----- 66
Db 8 GLWLAV---VTKRGPSASGSRGSS-----LCTGCTA-----CIGDLPGLLSLS 50
XX
Qy 67 ----CAAAPAPPRLL--WPILGGLSLTFVLGLL 95
Db 51 LLLVCSIAPISSSRIALAKLPRVGFPMEEAVYRGIL 86
XX
RESULT 14
AAU57190
ID AAU57190 standard; protein; 114 AA.
XX
XX AAU57190;
XX
XX 27-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #18086.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59580.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 18385; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
```


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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:10:21 ; Search time 127 Seconds
(without alignments)
293.302 Million cell updates/sec

Title: US-10-062-831-59

Perfect score: 608

Sequence: 1 MARGSLRLRLVGLWLA.....LSGFLVWRCRRSSPPX 114

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Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 626400

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	608	100.0	114	14	US-10-062-831-59
2	608	100.0	114	15	US-10-062-831-59
3	274.5	45.1	112	15	US-10-351-334-139
4	74.5	12.3	112	16	US-10-437-963-108148
5	70	11.5	70	15	US-10-380-703-27
6	69.5	11.4	109	15	US-10-425-114-61480
7	68	11.2	70	15	US-10-380-703-21
8	68	11.2	70	15	US-10-380-703-30
9	67.5	11.1	72	16	US-10-437-963-163452
10	67	11.0	70	15	US-10-380-703-26
11	67	11.0	74	10	US-09-468-147-190
12	67	11.0	74	15	US-10-319-745-190
13	66	10.9	70	15	US-10-380-703-19

Sequence 28, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 28395, A
Sequence 31337, A
Sequence 210769,
Sequence 153296,
Sequence 20, Appl
Sequence 23, Appl
Sequence 29, Appl
Sequence 53, Appl
Sequence 175619,
Sequence 189725,
Sequence 36263, A
Sequence 13, Appl
Sequence 25, Appl
Sequence 152927,
Sequence 217717,
Sequence 50873, A
Sequence 179616,
Sequence 191164,
Sequence 8362, Ap
Sequence 43778, A
Sequence 215, App
Sequence 215, App
Sequence 215, App
Sequence 215, App
Sequence 215, App
Sequence 334, App
Sequence 334, App

ALIGNMENTS

RESULT 1

US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: 32 Human Secreted Proteins
; APPLICANT: Steven M. Ruben, et al.
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114

;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match 100.0%; Score 608; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
|
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
|
Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 114
|
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 114
|

RESULT 2

US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match 100.0%; Score 608; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
|

Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 114
|
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 114
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RESULT 3

US-10-351-334-139
; Sequence 139, Application US/10351334
; Publication No. US20040034196A1
; GENERAL INFORMATION:
; APPLICANT: Komatsoulis et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/095,454
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 60/095,455
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-334-139

Query Match 45.1%; Score 274.5; DB 15; Length 112;
Best Local Similarity 96.4%; Pred. No. 1.8e-16;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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|
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC 56
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RESULT 4

US-10-437-963-108148
; Sequence 108148, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108148
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1242C.1.pcp

US-10-437-963-108148

Query Match 12.3%; Score 74.5; DB 16; Length 112;
Best Local Similarity 34.5%; Pred. No. 17;
Matches 20; Conservative 8; Mismatches 17; Indels 13; Gaps 3;
QY 59 PHSD--FCLGCAAPAPPRLLWPIGGALSLTFLVGLLSGFLVWRCRRSSPPX 114
DB 3 PHDSIFLLGAAHQPRP-----PVVSNALT-----KLEVMAPRRRKQKHCPQP 49

RESULT 5

US-10-380-703-27
; Sequence 27, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-27

Query Match 11.5%; Score 70; DB 15; Length 70;
Best Local Similarity 32.2%; Pred. No. 28;
Matches 19; Conservative 6; Mismatches 28; Indels 6; Gaps 2;
QY 23 RSVAGEQAGTAPCSRGSWSADLDKCMDCASCRA-RPHSDFCLGCAAPAPPRLLWP 80
DB 5 RSLGRDAPPTPCNPAECFDALVRHVCAGLLTTPRKP-----AGASSPAPRTALQP 58

RESULT 6

US-10-425-114-61480
; Sequence 61480, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 61480
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-012-G11_FLI pep
US-10-425-114-61480

Query Match 11.4%; Score 69.5; DB 15; Length 109;
Best Local Similarity 29.7%; Pred. No. 48;
Matches 27; Conservative 9; Mismatches 36; Indels 19; Gaps 5;
QY 5 SLRLRLRLVLGLMLALLRSVAGEQAGTAPCSRGSWSADLD---KCMDCASCRCARPHS 61
DB 20 SMPILRYLFTL-----NNVAFCSVDRLDYGVSIMARNCRALRSQSHT 66

QY 62 DF-CLGC-AAAPPAPPRLLW-PIGGALSLT 89
DB 67 RIRCAACLSAADPQPHDLCNSFYNGRALCMT 97

RESULT 7

US-10-380-703-21
; Sequence 21, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (23)..(23)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-21

Query Match 11.2%; Score 68; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 44;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;
QY 23 RSVAGEQAGTAPCSRGSWSADLDKCMDCASCRA-RPHSDFCLGCAAPAPPRLLWP 80
DB 5 RSLGRDAPPTPCNPAECFDPLVRHVCAGLLTTPRKP-----AGASSPAPRTALQP 58

RESULT 8
US-10-380-703-30
; Sequence 30, Application US/10380703

Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; PRIOR FILING DATE: 2003-07-28
; PRIOR FILING DATE: 2003-07-28
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; FEATURE:
; OTHER INFORMATION: substitution
; NAME/KEY: VARIANT
; LOCATION: (23)..(23)
; OTHER INFORMATION: substitution
US-10-380-703-30
Query Match 11.2%; Score 68; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 44;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;
Qy 23 RSVAGEQAPGTAPCGSGSSWSADLDKCMDCASCRA-RPHSDFCLGCGAAAPAPFRLLP 80
Db 5 RSLGRDAPPTPCNQAECFOLLVHVCACGLLTTPRKP-----AGASSPAPRTALQP 58
RESULT 9
US-10-437-963-163452
; Sequence 163452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163452
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: substitution
US-10-437-963-163452
Query Match 11.1%; Score 67.5; DB 16; Length 72;
Best Local Similarity 28.9%; Pred. No. 50;
Matches 24; Conservative 16; Mismatches 26; Indels 17; Gaps 5;

Qy 37 SRGSSWSADLDKCMDCASCRA-RPHSDFCLGCGAAAP-----PAPFRLLPILGALSITF 90
Db 1 SLGSAPARRIYQSWDQCATVRAIPYA--VGGCVATPQFHEVPGTI-YLYPWNIAISVIT- 56
Qy 91 VLGLLSGFLVWRRCRRERSPPPP 113
Db 57 -----FSIWRVLKRTGISGP 72
RESULT 10
US-10-380-703-26
; Sequence 26, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR FILING DATE: 2003-07-28
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-26
Query Match 11.0%; Score 67; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 54;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;

Qy 23 RSVAGEQAPGTAPCGSGSSWSADLDKCMDCASCRA-RPHSDFCLGCGAAAPAPFRLLP 80
Db 5 RSLGRDAPPTPCNQAECFOLLVHVCACGLLTTPRKP-----AGASSPAPRTALQP 58
RESULT 11
US-09-468-147-190
; Sequence 190, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: HEPATITIS E VIRUS
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199

; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Hepatitis E Virus
; FEATURE:
; OTHER INFORMATION: z12-orf3.pep
US-09-468-147-190

Query Match 11.0%; Score 67; DB 10; Length 74;
Best Local Similarity 28.2%; Pred. No. 57;
Matches 24; Conservative 14; Mismatches 21; Indels 26; Gaps 5;
QY 30 APGTAPCSGSSWSADLDKCMDCASCRARPHSDFCGLGCAAAAPPAPFRLWPILGALSIT 89
Db 8 SPMGSPCALG-----LFCC--CSSC-----FCLCCPRHPA--SRLAAVVGAAAVP 50
QY 90 FVLGLSLGFLVWRRCRERSPPPX 114
Db 51 AVVSGVTGLIL-----SPSPS 66

RESULT 12
US-10-319-745-190
; Sequence 190, Application US/10319745
; Publication No. US20030211467A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/10/319,745
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US/09/468,147A
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/173,141
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/061,199
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Hepatitis E Virus
; FEATURE:
; OTHER INFORMATION: z12-orf3.pep
US-10-319-745-190

Query Match 11.0%; Score 67; DB 15; Length 74;
Best Local Similarity 28.2%; Pred. No. 57;
Matches 24; Conservative 14; Mismatches 21; Indels 26; Gaps 5;
QY 30 APGTAPCSGSSWSADLDKCMDCASCRARPHSDFCGLGCAAAAPPAPFRLWPILGALSIT 89
Db 8 SPMGSPCALG-----LFCC--CSSC-----FCLCCPRHPA--SRLAAVVGAAAVP 50
QY 90 FVLGLSLGFLVWRRCRERSPPPX 114
Db 51 AVVSGVTGLIL-----SPSPS 66

RESULT 13
US-10-380-703-19
; Sequence 19, Application US/10380703
; Publication No. US20040072188A1

; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (23)..(23)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(24)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-19

Query Match 10.9%; Score 66; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 67;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;
QY 23 RSVAGEAPGTAPCSGSSWSADLDKCMDCASCRARPHSDFCGLGCAAAAPPAPFRLWPI 80
Db 5 RSLGRDAPAPTPCQTECFDPLVRHCVACGLLTPTPKP-----AGASSAPPTALQP 58

RESULT 14
US-10-380-703-28
; Sequence 28, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 70

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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:59:26 ; Search time 42 Seconds
(without alignments)
202.619 Million cell updates/sec

Title: US-10-062-831-59
Perfect score: 608
Sequence: 1 MARGSLRRLRLVGLWLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 338531

Minimum DB seq length: 0
Maximum DB seq length: 114

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	608	100.0	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	68	11.2	112	4	US-09-252-991A-21707
4	64	10.5	95	4	US-09-252-991A-16640
5	63	10.4	73	4	US-09-270-767-36705
6	63	10.4	73	4	US-09-270-767-51922
7	61.5	10.1	79	4	US-09-513-999C-4659
8	61.5	10.1	80	4	US-09-471-276-813
9	61.5	10.1	95	4	US-09-621-976-5253
10	61	10.0	71	4	US-09-107-532A-4242
11	60.5	10.0	75	6	5189019-4
12	60.5	10.0	75	6	5189019-4
13	60.5	10.0	94	3	US-08-851-843A-215
14	60.5	10.0	94	3	US-08-974-549A-334
15	60.5	10.0	94	3	US-08-854-050-215
16	60.5	10.0	94	3	US-09-430-323-215
17	60.5	10.0	94	4	US-09-402-181B-334
18	60.5	10.0	94	4	US-09-721-456-334
19	60.5	10.0	108	4	US-09-270-767-35067
20	60.5	10.0	108	4	US-09-270-767-50284
21	60	9.9	93	4	US-09-270-767-35319
22	60	9.9	93	4	US-09-270-767-50536
23	60	9.9	109	4	US-09-252-991A-29444
24	59.5	9.8	71	4	US-09-252-991A-26803
25	59.5	9.8	99	4	US-09-252-991A-25315
26	59.5	9.8	103	4	US-09-489-039A-7227
27	59	9.7	68	1	US-07-696-051B-1

28	59	9.7	68	1	US-07-924-063A-1	Sequence 1, Appli
29	59	9.7	68	1	US-08-138-340B-2	Sequence 2, Appli
30	58.5	9.6	69	4	US-09-205-258-439	Sequence 439, App
31	58	9.5	98	4	US-09-252-991A-31510	Sequence 31510, A
32	58	9.5	111	4	US-09-252-991A-17821	Sequence 17821, A
33	57.5	9.5	82	4	US-09-107-433-3031	Sequence 3031, Ap
34	57.5	9.5	96	4	US-09-252-991A-23413	Sequence 23413, A
35	57.5	9.5	104	4	US-09-252-991A-23645	Sequence 23645, A
36	57.5	9.5	110	4	US-09-252-991A-18800	Sequence 18800, A
37	57	9.4	48	4	US-09-471-276-1121	Sequence 1121, Ap
38	57	9.4	102	4	US-09-252-991A-22067	Sequence 22067, A
39	56.5	9.3	100	4	US-09-127-578-6	Sequence 6, Appli
40	56.5	9.3	111	4	US-09-252-991A-23578	Sequence 23578, A
41	56	9.2	85	1	US-08-468-347-18	Sequence 18, Appl
42	56	9.2	85	2	US-08-467-389-18	Sequence 18, Appl
43	56	9.2	85	2	US-08-779-379-18	Sequence 18, Appl
44	56	9.2	85	2	US-08-469-219-18	Sequence 18, Appl
45	56	9.2	85	3	US-09-228-152-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-690-454-59
; Sequence 59, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59

Query Match 100.0%; Score 608; DB 4; Length 114;
Best Local Similarity 100.0%; Pred.No. 6e-58;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVGLWLAIRSVAGEQAPCTAPCSGSSWSADLDKCMDCASCARAPH 60
DB 1 MARGSLRRLRLVGLWLAIRSVAGEQAPCTAPCSGSSWSADLDKCMDCASCARAPH 60


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US-09-270-767-51922
; Sequence 51922, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51922
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-51922

Query Match      10.4%; Score 63; DB 4; Length 73;
Best Local Similarity 22.0%; Pred. No. 13;
Matches 20; Conservative 7; Mismatches 20; Indels 44; Gaps 3;

QY 24 SVAGQAPGTCPSGSSWSADLCKMDCASCRCRPHSDFCIGCAAPAPRLWPILG 83
Db 27 AVAGDRGTGVNARDW---LHQC-----AFANHPPEP----- 58

QY 84 GALSITFVLGLSGLFVWRRCRRSSPPX 114
Db 59 -----RWENCHLEPAALPPG 73

RESULT 7
US-09-513-999C-4659
; Sequence 4659, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4659
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
; OTHER INFORMATION: seq SLPLLLLLGAWA/IP
US-09-513-999C-4659

Query Match      10.1%; Score 61.5; DB 4; Length 79;
Best Local Similarity 29.5%; Pred. No. 21;
Matches 23; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 10 LRLVLGLWLLRLRSVAGEQAPGTAPCSR---GSSWSADLCKMDCASCRCRPHSDFCIG 66
Db 7 LLLLLLGAW--AIPGGLGRAPLTATAPQLDDEMYSAHMPAHLKDCACRAVAYO----- 59

QY 67 CAAPAPPAPF--RLLWPIL 82
Db 60 ---VSPSPSPALLTPLL 74

RESULT 8
US-09-471-276-813
; Sequence 813, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 813
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
US-09-471-276-813

Query Match      10.1%; Score 61.5; DB 4; Length 80;
Best Local Similarity 29.5%; Pred. No. 21;
Matches 23; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 10 LRLVLGLWLLRLRSVAGEQAPGTAPCSR---GSSWSADLCKMDCASCRCRPHSDFCIG 66
Db 7 LLLLLLGAW--AIPGGLGRAPLTATAPQLDDEMYSAHMPAHLKDCACRAVAYO----- 59

QY 67 CAAPAPPAPF--RLLWPIL 82
Db 60 ---VSPSPSPALLTPLL 74

RESULT 9
US-09-621-976-5253
; Sequence 5253, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5253
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-5253

Query Match      10.1%; Score 61.5; DB 4; Length 95;
Best Local Similarity 23.9%; Pred. No. 26;
Matches 26; Conservative 9; Mismatches 31; Indels 43; Gaps 5;

QY 9 LRLVLGLWLLRLRSVAGEQAPGTAPCSRSSWSADLCKMDCASCRCRPHSDFCIGCA 68
Db 1 MARFLTCTWLLLG--PGLLATVRAECQ-----DCATC----- 33

QY 69 AAPAPPFRLWPILGGALSLTFVL-----GLLSGLFVWRRCRRSSP 111
```


;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 215:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 94 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-851-843A-215

Query Match 10.0%; Score 60.5; DB 3; Length 94;
Best Local Similarity 34.0%; Pred. No. 32;
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;

QY 36 CSRGSSWSADLDKCMDCASCRAPHSDFCLGCAAPPPAPFRLLPILGGA 85
DB 6 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 48

RESULT 14
US-08-974-549A-334
; Sequence 334, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 334:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 94 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-974-549A-334

Query Match 10.0%; Score 60.5; DB 3; Length 94;
Best Local Similarity 34.0%; Pred. No. 32;
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;

QY 36 CSRGSSWSADLDKCMDCASCRAPHSDFCLGCAAPPPAPFRLLPILGGA 85
DB 6 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 48

RESULT 15
US-08-854-050-215
; Sequence 215, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-854-050-215

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Query Match      10.0%; Score 60.5; DB 3; Length 94;
Best Local Similarity 34.0%; Pred. NO. 32;
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;
Oy 36 CSRGSSWSADLDKCMDCASCRRPHSDFCLGCAAPPPAPFLLWPIILGGA 85
Db 6 CARGKWPFRPPPR-----CRALPAAEFCAPCCATTARC-CRWPRSCGA 48

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Search completed: February 14, 2005, 07:14:45
Job time : 43 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	59	34.7	228	2	S53504	extensin-like prot
2	55	32.4	289	2	T34688	probable lipoprote
3	54	31.8	462	2	T17480	endo-xylanase homo
4	54	31.8	556	2	C87609	sensor histidine k
5	54	31.8	647	2	JE0337	frizzled-1 protein
6	53	31.2	127	2	C85091	arabinogalactan-pr
7	53	31.2	461	2	T57511	hypothetical prote
8	52	30.6	499	2	T46923	hypothetical prote
9	52	30.6	538	2	P83622	probable permease
10	52	30.6	957	2	A47531	glutaryl aminopept
11	51.5	30.3	537	2	T02982	probable sucrose t
12	51	30.0	245	2	AD0753	flagellar biosynth
13	51	30.0	245	2	S78698	probable export pr
14	51	30.0	313	2	F75251	cytochrome C oxida
15	51	30.0	520	2	S70198	glycosyltransferas
16	50.5	29.7	432	2	I48343	interleukin-11 rec
17	50.5	29.7	451	2	P87407	probable phosphodi
18	50.5	29.7	581	2	T44942	cytochrome-c oxida
19	50.5	29.7	625	2	B96710	hypothetical prote
20	50	29.4	133	2	C86473	arabinogalactan-pr
21	50	29.4	220	2	A75362	hypothetical prote
22	50	29.4	343	2	D75370	hypothetical prote
23	50	29.4	364	2	B72672	hypothetical prote
24	50	29.4	394	2	T04631	hypothetical prote
25	50	29.4	486	2	S71583	1-aminocyclopropan
26	50	29.4	626	2	H87648	cell division prot
27	49.5	29.1	379	2	D91078	probable lipoprote
28	49.5	29.1	379	2	E85923	lipoprotein D impor
29	49.5	29.1	379	2	B55522	lipoprotein D prec

RESULT 3

Tl7480
endo-xyylanase homolog PCZA361.l14 - Amycolatopsis orientalis
C:Species: Amycolatopsis orientalis
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: Tl7480
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, N.
Chem. Biol. 3, 155-162, 1998
A>Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin
A:Reference number: Z18904
A:Accession: Tl7480
A>Status: preliminary; translated from GS/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-462 <NAN>
A:Cross-references: UNIPROT.O52801; EMBL.AJ223998; NID:e1251208; PID:e1251219; PIDN:CAAL

Query Match 31.8%; Score 54; DB 2; Length 462;
Best Local Similarity 44.8%; Pred.No.16;
Matches 13; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 6 LRRLRLVLGLWLLALLRSVAGEQAQGTA 34
:|||||:|:|:|:|:|:|:
Db 1 MRRLALIVAGLSLVLPAAQAQPRAA 29

RESULT 4

C87609
sensor histidine kinase, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87609
B:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; UID:21173698; PMID:11259647
A:Accession: C87609
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-556 <STO>
A:Cross-references: UNIPROT.Q9A4C7; GB:AE005673; NID:gl3424529; PIDN:AAK24871.1; GSPDB:G
C:Gene: CC23909

```

Query Match      31.8%; Score 54; DB 2; Length 556;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 LRLVLVLGLWLTALLRS 24
      | | | | | | | | | |
Db      293 LLLLVLVLGLWLTALVYS 307

RESULT 5 ;
FE0337
Frizzled-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JE0337
R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoch, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A>Title: Molecular cloning, differential expression, and chromosomal localization of human
A:Reference number: JE0337; MUID:99032814; PMID:9813155
A:Accession: JE0337
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-647 <SAG>
A:Cross-references: UNIPROT:Q9UP38; DDBJ:AB017363; NID:G3927982; PIDN:EAA34666.1; PID:G3
C:Superfamily: fruit fly frizzled protein

Query Match      31.8%; Score 54; DB 2; Length 647;

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```

Best Local Similarity 42.9%; Pred.No. 21;
Matches 15; Conservative 3; Mismatches 11; Indels 6; Gaps 1;

QY 7 RRLRLVLGLWLAL-----LRSVAGEQAPGTAP 35
    |||||:|||||
Db 49 RRLARQLLLLELLEAPLLGLGVRAQAAGQPGQGP 83
    |||||:|||||

RESULT 6
C85091
arabinogalactan-protein homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85091
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The C
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
A:Reference number: A85001, MUID:20083488; PMID:10617198
A:Accession: C85091
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <STO>
A:Cross-references: UNIPROT:Q9W0S4; GB:NC_001268; NID:g7267545; PIDN:CAB78027.1
C:Genetics:
A:Gene: AT4g09030
A:Map position: 4

```

```

Query Match      31.2%; Score 53; DB 2; Length 127;
Best Local Similarity 56.5%; Pred. No. 7;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      13 LVVLGLLALLRSVAGEQAPGTP 35
      :|:|:|:|:|:|:|:|:|
DB       6 VVVLFLALLIASSAIAQAPGP 28

RESULT 7
S75711
hypothetical protein slr0896 - Synecchocystis sp. (strain PCC 6803)
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75711
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miya-
  o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Syne-
  c.

```

B. Reference number: S74322; MUID: 97061201; PMID: 8905231
 A.Accession: S57111
 A.Status: nucleic acid sequence not shown; translation not shown
 A.Organism: *Escherichia coli*
 A.Reading frame type: 61
 A.Reading frame: 1
 C.Reading references: UNIPROT_Q55364; EMBL_D64003; GB:AB001339; NID:G1001200; PMID:10552122
 A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 19 1997
 C.Superfamily: conserved hydrothermal protein H11612

```

Query Match      31.2%; Score 53; DB 2; Length 461;
Best Local Similarity 45.8%; Pred. No. 21;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      4  GSLRRLLRLVLGLWLLALLRSVAG 27
      | | | | : | | | | | | | |
Db      85  GQTRRIGQLTRQGLWIVLLLSIPG 108

RESULT 8
T46923
hypothetical protein DKFZp434E1512.1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C:Accession: T46923
R:Ducrestherhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S.

```


submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24138
A:Accession: T46923
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-499 <AAA>
A:CROSS-references: UNIPROT:Q43292; EMBL:AL157437
A:Experimental source: adult testis; clone DKF2p434E1512
C:Genetics:
A:Note: DKF2p434E1512.1

Query Match 30.6%; Score 52; DB 2; Length 499;
Best Local Similarity 41.2%; Pred. No. 31;
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 2 ARGSLRLRLVGLGLWLLALLRSVAGEQAPGTP 35
DB 255 AVGFLLVGLKALSLMQLHEAGMGLPEPGAP 288

RESULT 9

F83622
Probable permease of ABC transporter PA0185 [imported] - Pseudomonas aeruginosa (strain C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83622
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: F83622
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <STO>
A:CROSS-references: UNIPROT:Q916U8; GB:AE004456; GB:AE004091; NID:g9946013; PIDN:AAG0357
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0185

Query Match 30.6%; Score 52; DB 2; Length 538;
Best Local Similarity 48.4%; Pred. No. 33;
Matches 15; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

QY 5 SLRRLRLVGLGLWLLALLRSVAGEQAPGTP 35
DB 435 SLGEARVRLGFWRRRLRLV----LPGAAP 461

RESULT 10

A47531
Glutamyl aminopeptidase (EC 3.4.11.7) - human
N:Alternate names: aminopeptidase A; differentiation antigen gp160
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A47531; A48287
R:Li, L.; Wang, J.; Cooper, M.D.
Genomics 17, 657-664, 1993
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-957 <LIA>
A:CROSS-references: UNIPROT:Q07075; GB:IL12468; NID:g347892; PIDN:AAA16876.1; PID:g347893
R:Nanus, D.M.; Engelstein, D.; Gastl, G.A.; Gluck, L.; Vidal, M.J.; Morrison, M.; Finsta
Proc. Natl. Acad. Sci. U.S.A. 90, 7069-7073, 1993
A:Title: Molecular cloning of the human kidney differentiation antigen gp160: human aminopeptidase A
A:Reference number: A48287; MUID:93348214; PMID:8346219
A:Accession: A48287
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-217, 'A', 219-957 <NAN>
A:CROSS-references: GB:L14721; NID:g291853; PIDN:AAA35522.1; PID:g291854
C:Genetics:
A:Gene: GDB:ENPEP
A:CROSS-references: GDB:L38283; OMIM:L38297
A:Map position: 17pter-17p12
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Query Match 30.6%; Score 52; DB 2; Length 957;
Best Local Similarity 48.0%; Pred. No. 54;
Matches 12; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

QY 13 LVGLWLLALLRSV-AGEQAPGTP 35
DB 31 LIVGLAVGLTRSCDSSGDGPGTP 55

RESULT 11

T02982
Probable sucrose transport protein - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02982
R:Hirose, T.; Imaizumi, N.; Scofield, G.N.; Furbank, R.T.; Ohsugi, R.
Plant Cell Physiol. 38, 1389-1396, 1997
A:Title: cDNA cloning and tissue specific expression of a gene for sucrose transporter f
A:Reference number: Z14809; MUID:98182940; PMID:9522469
A:Accession: T02982
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-537 <HTR>
A:CROSS-references: UNIPROT:O49838; EMBL:D87819; NID:g2723470; PIDN:BAA24071.1; PID:g272
A:Experimental source: cultivar Nipponbare, leaf
C:Genetics:
A:Gene: SUT1
C:Superfamily: common tobacco sucrose transport protein

Query Match 30.3%; Score 51.5; DB 2; Length 537;
Best Local Similarity 35.3%; Pred. No. 38;
Matches 12; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

QY 14 VLGLWL-----ALLRSVAGEQAPGTA 34
DB 169 VLGFWLLDFSNNTVQGPAPALMADLSGRHGP 202

RESULT 12

AD0753
flagellar biosynthetic protein Flp [imported] - Salmonella enterica subsp. enterica ser
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0753
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <PAR>
A:CROSS-references: GB:ALU513382; PIDN:CAD05727.1; PID:GL65032220; GSPDB:GN00176
C:Genetics:
A:Gene: STY2187
C:Superfamily: flagellar biosynthetic protein flp

Query Match 30.0%; Score 51; DB 2; Length 245;
Best Local Similarity 48.1%; Pred. No. 23;
Matches 13; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 6 LRRLLRLVLGLWLLALRSVAGEQAPG 32
Db 1 MRRLLFLSLAGLW--LFSFAAAQLPG 25

RESULT 13

S78698

probable export protein flip precursor - Salmonella typhimurium

C:Species: Salmonella typhimurium

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C:Accession: S78698

R:Ohnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 179, 6092-6099, 1997

A:Title: The FlpO, FlpP, and FlpR proteins of Salmonella typhimurium: putative com

A:Reference number: S78696; MUID:97464436; PMID:9324257

A:Accession: S78698

A:Molecule type: DNA

A:Residues: 1-245 <OHN>

A:Cross-references: UNIPROT:P54700; EMBL:L49021; NID:g1066860; PIDN:AAB81319.1; PID:g106

A:Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are

C:Genetics:

A:Gene: flip

C:Function:

A:Description: may be involved in flagellar assembly; may be involved in export of flag

C:Superfamily: flagellar biosynthetic protein flip

C:Keywords: flagellum; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-245/Product: probable export protein flip #status predicted <MAT>

F:45-61/Domain: transmembrane #status predicted <TM1>

F:89-105/Domain: transmembrane #status predicted <TM2>

F:189-205/Domain: transmembrane #status predicted <TM3>

F:212-228/Domain: transmembrane #status predicted <TM4>

Query Match 30.0%; Score 51; DB 2; Length 245;

Best Local Similarity 48.1%; Pred. No. 23;

Matches 13; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 6 LRRLLRLVLGLWLLALRSVAGEQAPG 32

Db 1 MRRLLFLSLAGLW--LFSFAAAQLPG 25

RESULT 14

F75251

cytochrome C oxidase assembly factor - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: F75251

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75251

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-313 <WHI>

A:Cross-references: UNIPROT:Q9RR78; GB:AE002091; GB:AE000513; NID:g6460446; PIDN:AAF1215

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2618

A:Map position: 1

C:Superfamily: heme O synthase

Query Match

Best Local Similarity 30.0%; Score 51; DB 2; Length 313;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 16 GLWLLALRSVAGEQAPGTA 34

Db 56 GLWLLIVVSVAGYMSAGSA 74

RESULT 15

S70198

glycosyltransferase homolog kfic [imported] - Escherichia coli

C:Species: Escherichia coli

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S70198; S70193

R:Petit, C.; Rigg, G.; Fazzani, C.; Smith, A.; Sieberth, V.; Stevens, M.; Boulnois, G.;

submitted to the EMBL Data Library, February 1994

A:Description: Region 2 of the Escherichia coli K5 capsule gene cluster encoding protein

A:Reference number: S70198

A:Accession: S70198

A:Molecule type: DNA

A:Residues: 1-520 <PET>

A:Cross-references: UNIPROT:Q47330; EMBL:X77617; NID:g496601; PIDN:CAA54709.1; PID:g7359

R:Petit, C.; Rigg, G.P.; Pazzani, C.; Smith, A.; Sieberth, V.; Stevens, M.; Boulnois, G.

Mol. Microbiol. 17, 611-620, 1995

A:Title: Region 2 of the Escherichia coli K5 capsule gene cluster encoding proteins for

A:Reference number: S70191; MUID:96111482; PMID:8801416

A:Accession: S70193

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 279-316, 318-362 <PEW>

A:Cross-references: EMBL:X77617

C:Genetics:

A:Gene: kfic

Query Match

Best Local Similarity 30.0%; Score 51; DB 2; Length 520;

Matches 14; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 3 RGSRLRLRLVLGLW--LALLRSVAGEQAP 31

Db 440 RESIVRLQLLGLWGDSGLTRNKGTEALP 470

Search completed: February 10, 2005, 18:20:10

Job time : 12.2851 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:01:53 ; Search time 50.1974 Seconds
(without alignments)
357.046 Million cell updates/sec

Title: US-10-062-831-59_COPY_1_35

Perfect score: 170

Sequence: 1 MARGSLRLRLVGLMLALLRSVAGEAPGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	129	1 FN14 HUMAN	Q9np84 homo sapien
2	96	56.5	129	2 Q80XK9	Q80xx9 rattus norv
3	92	54.1	129	1 FN14 MOUSE	Q9cr75 m tumor nec
4	60	35.3	466	2 Q89W72	Q89w72 bradyrhizob
5	60	35.3	508	2 Q8W616	Q8w616 sinorhizobi
6	59	34.7	228	2 Q43558	Q43558 medicago sa
7	59	34.7	401	2 Q97407	Q97407 anopheles g
8	58	34.1	577	2 Q8S922	Q8s922 oryza sativ
9	58	34.1	577	2 Q6RU76	Q6ru76 oryza sativ
10	58	34.1	577	2 Q6VEF4	Q6vef4 oryza sativ
11	57	33.5	986	2 Q6L8S8	Q6l8s8 mus musculu
12	56	32.9	173	2 Q9JXD5	Q9jxd5 rattus norv
13	56	32.9	300	2 Q9JHY1	Q9jhy1 rattus norv
14	55	32.4	289	2 Q69838	Q69838 streptomyce
15	55	32.4	300	2 Q8VC39	Q8vc39 mus musculu
16	55	32.4	465	2 Q82B13	Q82b13 streptomyce
17	55	32.4	527	2 Q82A33	Q82a33 drosophila
18	55	32.4	572	2 Q9W2P2	Q9w2p2 drosophila
19	55	32.4	873	2 Q98949	Q98949 gallus gall
20	55	32.4	962	2 Q87055	Q87055 ralatstonia s
21	54.5	32.1	809	2 Q66DL4	Q66dl4 versinia ps
22	54.5	32.1	823	2 Q8WY18	Q8wy18 homo sapien
23	54.5	32.1	823	2 Q8CE84	Q8ce84 mus musculu
24	54.5	32.1	1188	1 ITAH MOUSE	P61622 mus musculu
25	54.5	32.1	1188	2 Q7TQC3	Q7tqc3 mus musculu
26	54.5	32.1	1189	1 ITAH HUMAN	Q9ukx5 homo sapien
27	54	31.8	95	2 Q9AX04	Q9ax04 oryza sativ
28	54	31.8	300	1 JAM1 MOUSE	Q88792 mus musculu
29	54	31.8	401	2 Q7QFQ0	Q7qfq0 anopheles g
30	54	31.8	404	2 Q82C69	Q82c69 streptomyce
31	54	31.8	418	2 Q91AF4	Q91af4 bacillus sp

32 54 31.8 462 2 052801
33 54 31.8 528 2 062K31
34 54 31.8 556 2 09A4C7
35 54 31.8 648 1 FZD1 HUMAN
36 54 31.8 3908 2 Q7N4L0
37 53 31.2 127 2 Q9M0S4
38 53 31.2 153 2 Q9UB33
39 53 31.2 178 2 Q6AQM2
40 53 31.2 371 2 Q8PJ04
41 53 31.2 461 1 NORM SYN3
42 53 31.2 539 2 Q70I04
43 53 31.2 573 2 Q758D4
44 53 31.2 661 2 Q8QVL2
45 53 31.2 678 2 Q94798

052801 amycolatops
062k31 burkholderi
09a4c7 caulobacter
09up38 homo sapien
07n4l0 photornadu
09m0s4 arabidopsis
09ub33 anopheles g
06aqm2 desulfotale
08pj04 xanthomonas
055364 synechocyst
Q70i04 streptomyce
Q758d4 ashbya goss
Q8qvl2 hamster par
Q94798 trypanosoma

ALIGNMENTS

RESULT 1

FN14_HUMAN STANDARD; PRT; 129 AA.
AC Q9NP84; Q9HC50;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member FN14 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).
GN Name=TNFRSF12A; Synonyms=FN14;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=20216634; PubMed=10751351;
RA Feng S.-L.Y., Guo Y., Factor V.M., Thorgerisson S.S., Bell D.W.,
RA Testa J.R., Peifley K.A., Winkles J.A.;
RT "The FN14 immediate-early response gene is induced during liver
RT regeneration and highly expressed in both human and murine
RT hepatocellular carcinomas."
RL Am. J. Pathol. 156:1253-1261(2000).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Tanaka S., Sugimachi K.;
RT "Human homologue of FN14."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Uterus;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

RN FUNCTION.
RP MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;
RX Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RT "A novel TNF receptor family member binds TWEAK and is implicated in
RT angiogenesis.";
RL Immunity 15:837-846(2001).
CC -!- FUNCTION: Receptor for TNFRSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_006519;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC -!- INDUCTION: By FGF-1 and phorbol ester.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF191148; AAF69108.1; -;
DR EMBL; AB035480; BAA94792.1; -;
DR EMBL; AB035481; BAB17850.1; -;
DR EMBL; BC002718; BAA02718.1; -;
DR H-InvDB; HGNC:18152; TNFRSF12A.
DR MIM; 605914; -;
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007275; P:development; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00050; TNFR_NGFR_2; FALSE NEG.
KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT FT superfamily member Fnl4.
FT FT Extracellular (Potential).
FT FT Potential.
FT FT Cytoplasmic (Potential).
FT FT TNFR-Cys (atypical).
FT FT Potential.
FT FT Potential.
FT FT Missing (in isoform 2).
FT FT /FTID=VSP_006519.
SQ SEQUENCE 129 AA; 13911 MW; BF3DFB9C1E1C448 CRC64;

Query Match 100.0%; Score 170; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAP 35
Db 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAP 35

RESULT 2
Q80XX9
```

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ID Q80XX9 PRELIMINARY; PRT; 129 AA.
AC Q80XX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type 1 transmembrane protein Fnl4 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller A.M., Giegerich G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Pituitary gland;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Pituitary gland;
RX Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY255102; AAP06753.1; -;
DR EMBL; BC060537; BAA60537.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002212; Fibril-assoc.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match 56.5%; Score 96; DB 2; Length 129;
Best Local Similarity 62.9%; Pred. No. 6.1e-05;
Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Oy 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAP 35
Db 1 MAPCPWPRPLQLLVGLGLVLRATAGEQAPGNAP 35

RESULT 3
Fnl4 MOUSE
ID Fnl4 MOUSE STANDARD; PRT; 129 AA.
AC Q9CR75; Q9QZK3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member Fnl4 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)
DE (Tweak-receptor) (TweakR).
GN Name=tnfrsf12a; Synonyms=Egfrp2, Fnl4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=BALB/c; TISSUE=Fibroblast;
CC MEDLINE=2020297; PubMed=10551889; DOI=10.1074/jbc.274.46.33166;
CC Meignan-Mantha R.D., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,
CC Feifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
CC Richards C.M., Winkles J.A.;
CC "The mitogen-inducible Fn14 gene encodes a type I transmembrane
CC protein that modulates fibroblast adhesion and migration.";
CC J. Biol. Chem. 274:33166-33176(1999).
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;
CC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01326;
CC Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
CC Nikaido I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
CC Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
CC Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
CC Blake J.A., Bradt D., Brusic V., Chochia L.C., Corbani L.E., Cousins S.,
CC Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
CC Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
CC Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
CC Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
CC Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
CC Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,
CC Nagashima T., Numa K., Okido T., Pavan W.J., Perteza G.,
CC Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
CC Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
CC Sanderlin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
CC Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
CC Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
CC Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
CC Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
CC Hirozane-Hashikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
CC Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
CC Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
CC Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
CC Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
CC Birney E., Hayashizaki Y.;
CC "Analysis of the mouse transcriptome based on functional annotation of
CC 60,770 full-length cDNAs.";
CC Nature 420:563-573(2002).
CC [3]
CC SEQUENCE FROM N.A.
CC TISSUE=Breast tumor;
CC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
CC Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
CC Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
CC Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
CC "Generation and initial analysis of more than 15,000 full-length human
CC and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC [1]
CC FUNCTION: Receptor for TNFSF12/TWEAK (By similarity). Weak inducer
CC of apoptosis in some cell types. Promotes angiogenesis and the
CC proliferation of endothelial cells. May modulate cellular adhesion
CC to matrix proteins.

```
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005937; C:membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:antiporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0008655; P:multidrug transport; IEA.
DR InterPro; IPR002528; Mate; 2.
DR Pfam; PF01554; Mate; 2.
DR TIGRFAMs; TIGR00797; mate; 1.
KW Complete proteome.
SQ SEQUENCE 466 AA; 49216 MW; BBD66F41E70E694A CRC64;

Query Match 35.3%; Score 60; DB 2; Length 466;
Best Local Similarity 46.4%; Pred. No. 15;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 GSLRLLRLVLGLWLLRLSVAGEQAP 31
DB 97 GGVRRIRRALRVGLWVALLISLPMWASP 124

RESULT 5
Q8W616 PRELIMINARY; PRT; 508 AA.
AC Q8W616;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein orf41.
GN Name=orf41;
OS Sinorhizobium meliloti phase PBC5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
OX NCBI_TaxID=179237;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmeister S.A., Krol J.E., Vorhoeelter F.-J., Skorupska A.M.,
RA Lotz W.;
RT "Sequence of the genome of Sinorhizobium meliloti bacteriophage
RT PBC5.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schmeister S.A., Krol J.E., Vorhoeelter F.-J., Skorupska A.M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448724; AAL49639.1; -.
KW Hypothetical protein.
SQ SEQUENCE 508 AA; 54579 MW; C61CE7A54EF600F5 CRC64;

Query Match 35.3%; Score 60; DB 2; Length 508;
Best Local Similarity 51.5%; Pred. No. 16;
Matches 17; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 4 GSLRLLRLVLGLWLLRLSVAGEQAP 32
DB 248 GGLRLLRLVLGLWLLRLSVAGEQAP 280

RESULT 6
Q43558 PRELIMINARY; PRT; 228 AA.
AC Q43558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Proline rich protein precursor.
OS Eukaryota; Viridiplantae;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
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RN SEQUENCE FROM N.A.
RP TISSUE=Stem;
RC MEDLINE=95201245; PubMed=7894016;
RX Abrahams S., Hayes C.M., Watson J.M.;
RT "Expression patterns of three genes in the stem of lucerne (Medicago
RT sativa).";
RL Plant Mol. Biol. 27:513-528(1995).
DR EMBL; L36120; AAB41815.1; -.
DR PIR; S53504; S53504.
KW Signal.
FT SIGNAL 1 7 Potential.
FT CHAIN 8 228 proline rich protein.
SQ SEQUENCE 228 AA; 22480 MW; 15CAAE63CC1F0532E CRC64;

Query Match 34.7%; Score 59; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 12 LLVLGLWLLRLSVAGEQAPGTAP 35
DB 7 VLVVGLICAVFSSVGAQAPSTSP 30

RESULT 7
Q97407 PRELIMINARY; PRT; 401 AA.
AC Q97407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SGI protein precursor.
GN Name=SGI;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RX MEDLINE=99145581; PubMed=990055; DOI=10.1073/pnas.96.4.1516;
RA Arca B., Lombardo F., de Lara Capurro M., della Torre A.,
RA Dinopoulos G., James A.A., Coluzzi M.;
RT "Trapping cDNAs encoding secreted proteins from the salivary glands of
RT the malaria vector Anopheles gambiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1516-1521(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RA Arca' B., Lombardo F., Capurro de Lara Guimaraes M., della Torre A.,
RA Dinopoulos G., James A.A., Coluzzi M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ130949; CAA10258.1; -.
KW Signal.
FT SIGNAL 1 14
SQ SEQUENCE 401 AA; 46277 MW; 22000EAB25CE8085 CRC64;

Query Match 34.7%; Score 59; DB 2; Length 401;
Best Local Similarity 55.0%; Pred. No. 17;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 LLVLGLWLLRLSVAGEQ 29
DB 1 MRLVLTIWIGCVNSTFGEQ 20

RESULT 8
Q8S922 PRELIMINARY; PRT; 577 AA.
AC Q8S922;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

DE Cell wall invertase (EC 3.2.1.26).
GN Names-Oscini;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Panicum;
RX MEDLINE=21975747; PubMed=11978873;
RA Hirose T.; Takano M.; Terao T.;
RT "Cell wall invertase in developing rice caryopsis: molecular cloning
of cscini and analysis of its expression in relation to its role in
grain filling."
RL Plant Cell Physiol. 43:452-459(2002).
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
DR EMBL; AB073749; BAB90855.1; -;
DR Gramine; Q8S922; -;
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001362; Glyco_hydro_32.
DR InterPro; IPR011040; Sialidase.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR SMART; SM00640; Glyco_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 577 AA; 63984 MW; 41PE6384284F97F1 CRC64;

Query Match 34.1%; Score 58; DB 2; Length 577;
Best Local Similarity 40.5%; Pred. No. 33;
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;

QY 11 RLLVLGLWLLI-----RSVAGEQAPGTAP 35
Db 4 RLLALAPWLLLLLQLAGASHVVRHSLEAEQAPSSVP 40
[1]

RESULT 9
Q6EU76 PRELIMINARY; PRT; 577 AA.
ID Q6EU76;
AC Q6EU76;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cell wall invertase 1.
GN Name=OJ112.G07.1; Synonyms=B1136H02.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
DR EMBL; AF004156; BAD27793.1; -;
DR EMBL; AF005798; BAD29294.1; -;
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001362; Glyco_hydro_32.
DR InterPro; IPR011040; Sialidase.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR SMART; SM00640; Glyco_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 577 AA; 63984 MW; 2A39D555E834529C CRC64;

Query Match 34.1%; Score 58; DB 2; Length 577;
Best Local Similarity 40.5%; Pred. No. 33;
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;

QY 11 RLLVLGLWLLI-----RSVAGEQAPGTAP 35
Db 4 RLLALAPWLLLLLQLAGASHVVRHSLEAEQAPSSVP 40
[1]

RESULT 10
Q6VEF4 PRELIMINARY; PRT; 577 AA.
ID Q6VEF4;
AC Q6VEF4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cell wall invertase 1 (EC 3.2.1.26).
GN Name=CIN1;
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Y.-Q., Zhu Z.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
DR EMBL; AY342319; AAQ24869.1; -;
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001362; Glyco_hydro_32.
DR InterPro; IPR011040; Sialidase.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR SMART; SM00640; Glyco_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 577 AA; 63984 MW; 2A39D555E834529C CRC64;

Query Match 34.1%; Score 58; DB 2; Length 577;
Best Local Similarity 40.5%; Pred. No. 33;
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;

QY 11 RLLVLGLWLLI-----RSVAGEQAPGTAP 35
Db 4 RLLALAPWLLLLLQLAGASHVVRHSLEAEQAPSSVP 40
[1]

RESULT 11
Q6L8S8 PRELIMINARY; PRT; 986 AA.
ID Q6L8S8;
AC Q6L8S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Betal, 4-N-acetyl-galactosaminyltransferase III.
GN Name=beta4GalNACT3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12966086; DOI=10.1074/jbc.M308857200;
RA Sato T., Gotoh M., Kiyohara K., Kameyama A., Kubota T., Kikuchi N.,
RA Ishizuka Y., Iwaseki H., Togayachi A., Kudo T., Ohkura T.,
RA Nakanishi H., Narimatsu H.;
RT "Molecular cloning and characterization of a novel human beta 1,4-N-
acetyl-galactosaminyltransferase, beta 4galNAC-T3, responsible for the
synthesis of N,N'-diacetyllactosamine, galNAC beta 1-4GlcNAc.";
RL J. Biol. Chem. 278:47534-47544(2003).
DR EMBL; AB114826; BAD02450.1; -;
DR GO; GO:0016740; F:transferase activity; IEA.


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KW Transference.
SQ SEQUENCE 986 AA; 113509 MW; D4CFB2B6B629A021 CRC64;

Query Match 33.5%; Score 57; DB 2; Length 986;
Best Local Similarity 48.5%; Pred. No. 75;
Matches 16; Conservative 1; Mismatches 10; Indels 6; Gaps 1;

QY 6 LRLRLRLVL-----GLWLALLRSVAGEQAPG 32
   ||| |||:| ||| ||| ||| ||| |||
DB 19 LRRRRLRLLLAVSVGLWTLYLELVASQAQGG 51

RESULT 12
Q9JKD5 PRELIMINARY; PRT; 173 AA.
AC Q9JKD5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule (fragment).
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirsch T., Wellner M., Haller H., Lippoldt A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241261; AAF61729.1; -.
DR HSSP; O88792; 1F97.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 173 AA; 18706 MW; 3EE3ECDF5A5FB8B2 CRC64;

Query Match 32.9%; Score 56; DB 2; Length 173;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 9 LRLRLVLGLLALLRSVAGEQAPGTAP 35
   ||| |||:| ||| ||| ||| |||
DB 122 LLGLLIFGIWFAYSRGYFERTKKGTP 148

RESULT 13
Q9JHY1 PRELIMINARY; PRT; 300 AA.
AC Q9JHY1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Junctional adhesion molecule JAM (Junctional adhesion molecule
DE 1).
GN Name=Jam; Synonyms=Jam1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashima H., Kojima I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276998; AAF78250.1; -.
DR EMBL; BC065309; AAH65309.1; -.
DR HSSP; O88792; 1F97.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;

Query Match 32.9%; Score 56; DB 2; Length 300;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 9 LRLRLVLGLLALLRSVAGEQAPGTAP 35
   ||| |||:| ||| ||| ||| |||
DB 249 LLGLLIFGIWFAYSRGYFERTKKGTP 275

RESULT 14
O69838 PRELIMINARY; PRT; 289 AA.
AC O69838;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative lipoprotein.
GN ORFNames=SC1B5.10c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939126; CAAL8984.1; -.
DR FIR; T34688; T34688.
DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. .; IEA.

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DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR002509; PolySacc deacet.
 DR Pfam; PF01522; PolySacc deac 1; 1.
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 289 AA; 30748 MW; 4484081584FCB3D07 CRC64;
 Query Match 32.4%; Score 55; DB 2; Length 289;
 Best Local Similarity 46.7%; Pred. No. 44;
 Matches 14; Conservative 2; Mismatches 14; Indels 0; Gaps 0;
 QY 6 LRLRLRLVLGLWLLALLRSVAGEQAPGTAP 35
 DB 5 VRRATALCVLGAALAAACGTTGAQPRAP 34
 RESULT 15
 Q8VC39 PRELIMINARY; PRT; 300 AA.
 AC Q8VC39;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Fllr protein (Mus musculus adult male cecum CDNA, RIKEN full-length
 DE enriched library, clone:9130004G24 product:junction cell adhesion
 DE molecule1, full insert sequence).
 GN Name=Fllr;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Maruskin K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).

RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayato M., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; EC021876; AAH21876.1; -.
 DR EMBL; AK033574; BAC28369.1; -.
 DR HSSP; O88792; 1F97.
 DR MGD; MGI:1321398; Fllr.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 SQ SEQUENCE 300 AA; 32423 MW; 3CE561E8FF3B97EC CRC64;
 Query Match 32.4%; Score 55; DB 2; Length 300;
 Best Local Similarity 44.4%; Pred. No. 45;
 Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 QY 9 LRLRLVLGLWLLALLRSVAGEQAPGTAP 35
 DB 249 LLGLLIFGVWFAYSGYFERTKGTAP 275

Search completed: February 10, 2005, 18:17:12
 Job time : 53.1974 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 17:53:53 ; Search time 55.5702 Seconds
(without alignments)
243.595 Million cell updates/sec

Title: US-10-062-831-59_COPY_1_35

Perfect score: 170

Sequence: 1 MARGSLRLRLRLVLLGLMLRLSVAGPQGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	100.0	112	3	AAY91463 Human sec
2	170	100.0	112	6	ADA57390 Human sec
3	170	100.0	112	7	ADC74462 Human sec
4	170	100.0	112	7	ADD38025 Human sec
5	170	100.0	112	8	ADL71535 Novel hum
6	170	100.0	114	2	AAW73409 Human sec
7	170	100.0	129	2	AAW88506 Human liv
8	170	100.0	129	3	AAV57940 Human tra
9	170	100.0	129	4	AAU03498 Human TWE
10	170	100.0	129	5	ABP61512 Human NF-
11	170	100.0	129	5	AAU79827 Human typ
12	170	100.0	129	6	ADA56889 Human sec
13	170	100.0	129	6	ABU56716 Lung canc
14	170	100.0	129	7	ADC74112 Human sec
15	170	100.0	129	7	ADD37867 Human sec
16	170	100.0	129	7	ADD89033 TAT274.1
17	170	100.0	129	7	ABU64232 Human FFA
18	170	100.0	129	7	ADN39126 Cancer/an
19	170	100.0	129	7	ADN39987 Cancer/an
20	170	100.0	129	8	ABM81706 Tumour-as
21	170	100.0	155	3	AAV91604 Human sec
22	170	100.0	155	6	ADA57391 Human sec
23	170	100.0	155	7	ADC74463 Human sec
24	170	100.0	155	7	ADD38026 Human sec
25	170	100.0	155	8	ADL71680 Novel hum

26	170	100.0	156	3	AAV91552 Human sec
27	170	100.0	156	8	ADL71624 Novel hum
28	170	100.0	309	4	AAU03500 Human TWE
29	158	92.9	94	7	ABU64233 Human CRY
30	97	57.1	129	5	AAU79828 Mouse typ
31	61	35.9	79	5	ABP06392 Human ORF
32	57	33.5	986	8	ADK43170 Mouse N-a
33	56.5	33.2	671	6	ABU31710 Protein e
34	55	32.4	300	8	ADR46581 Mouse jun
35	55	32.4	572	4	ABT70909 Drosophil
36	54.5	32.1	1120	6	ABT58365 Human NOV
37	54.5	32.1	1188	4	AAU14467 Human nov
38	54.5	32.1	1188	4	AAU14231 Human nov
39	54.5	32.1	1188	4	AAU50085 Human A25
40	54.5	32.1	1188	4	AAU50087 Murine A2
41	54.5	32.1	1188	5	AAU10552 Murine A2
42	54.5	32.1	1188	5	AAU10551 Human A25
43	54.5	32.1	1188	7	ADE09956 Novel pro
44	54.5	32.1	1189	3	AAU25582 ITGA11 pr
45	54.5	32.1	1189	4	ABG12949 Novel hum

ALIGNMENTS

RESULT 1
AAY91463
ID AAY91463 standard; protein; 112 AA.
XX AC AAY91463;
XX AC
XX 29-JUN-2000 (first entry)
XX DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
XX KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
XX KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
XX KW osteoparitic; antidiabetic; antibacterial; antidiabetic; antiaschma;
XX KW aniposporitic; cardiant; gene therapy; cancer; neurological disorder;
XX KW immune disease; inflammation; blood disorder; tumour; chromosome 16.
XX OS Homo sapiens.
XX PN WO200006698-A1.
XX XX
XX PD 10-FEB-2000.
XX PF 29-JUL-1999; 99WO-US017130.
XX XX
XX 30-JUL-1998; 98US-0094657P.
XX PR 05-AUG-1998; 98US-0095486P.
XX PR 06-AUG-1998; 98US-0095454P.
XX PR 06-AUG-1998; 98US-0095455P.
XX PR 12-AUG-1998; 98US-0096319P.
XX XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
XX PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
XX PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX XX
XX WPI; 2000-195282/17.
XX N-PSDB; AAA26358.
XX XX
XX New isolated human genes and the secreted polypeptides they encode,
XX PT useful for diagnosis and treatment of e.g. cancers, neurological
XX PT disorders, immune diseases, inflammation or blood disorders.
XX XX
XX Claim 11; Page 465; 634pp; English.

The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are

PD 08-MAY-2003;
XX
PF 19-MAR-2002; 2002WO-US008277.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-430516/40.
XX
XX N-PSDB; ADC73847.
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT hemopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
XX Claim 16; SEQ ID NO 1095; 2272pp; English.
XX
PS The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current inference is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 170; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
RESULT 4
ADD38025
ID ADD38025 standard; protein; 112 AA.
XX
AC ADD38025;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted protein #208.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
XX
OS Homo sapiens.
XX
FN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-140218/13.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 1; SEQ ID NO 507; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases, wound healing and disorders of epithelial cell
CC proliferation, immune disorders, cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein.
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 170; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
RESULT 5
ADL71535
ID ADL71535 standard; protein; 112 AA.
XX
AC ADL71535;
XX
DT 20-MAY-2004 (first entry)
XX
DE Novel human secreted protein seqid 139.
XX
KW antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; antilipemic; CNS; gynaecological; antiarthritic;
KW antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
KW immunosuppressive; antiallergic; cardiovascular; respiratory;
KW dermatological; antimicrobial; gastrointestinal; gene therapy;
KW neurodegenerative disease; behavioral disorder; inflammatory condition;
KW hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW respiratory disorder; pulmonary disorder; connective tissue disorder;
KW skin disorder; CNS disorder; congenital disorder; infectious disorder;
KW gastrointestinal disorder; human; secreted protein.

Query Match 100.0%; Score 170; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 7
AAW88506
ID AAW88506 standard; protein; 129 AA.
AC AAW88506;
XX
DT 30-MAR-1999 (first entry)
DE Human liver clone HP10432-encoded membrane protein.
KW Transmembrane protein; HP10432; human; liver.
OS Homo sapiens.
XX WO9855508-A2.
FN 10-DEC-1998.
XX
PD 03-JUN-1998; 98WO-JP002445.
XX
PR 03-JUN-1997; 97JP-00144948.
XX
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Sekine S, Yamaguchi T;
XX WPI; 1999-045730/04.
DR N-PSDB; AAV84374.
XX
PT New human proteins containing transmembrane domains and their encoding
PT sequences - useful in the preparation of antibodies and large-scale
PT protein production, gene diagnosis, and gene therapy.
XX
PS Claim 1; Page 152-153; 178pp; English.
XX
CC This is the amino acid sequence of a transmembrane protein encoded by
CC human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a
CC signal-like N-terminal region and one internal transmembrane domain. The
CC invention provides nucleotide sequences (see AAV84359-76) coding for 18
CC transmembrane proteins (see AAV88491-508), vectors containing such
CC polynucleotides, and eukaryotic cells containing the vectors. The
CC proteins can be used as antigens or as compositions in the preparation of
CC antibodies against the proteins. The polynucleotides can be used as
CC probes for gene diagnosis, and as gene sources for gene therapy and large
CC scale production of proteins encoded by the cDNA. The host cells are
CC used for the detection of ligands corresponding to the expressed
CC proteins, and the screening of low mol.wt. medicines

QY Sequence 129 AA;
Query Match 100.0%; Score 170; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 8
AAV57940
ID AAV57940 standard; protein; 129 AA.
XX

AC AAY57940;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human transmembrane protein HTMPN-64.
XX
KW Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
KW antiproliferative; neuroprotective; immune disorder;
KW reproductive disorder; smooth muscle disorder; neurological disorder;
KW gastrointestinal disorder; developmental disorder;
KW cell proliferative disorder.
XX
OS Homo sapiens.
XX WO9961471-A2.
FN
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011904.
XX
PR 29-MAY-1998; 98US-0087260P.
PR 02-JUL-1998; 98US-0091674P.
PR 02-OCT-1998; 98US-0102954P.
PR 24-NOV-1998; 98US-0109869P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
XX WPI; 2000-072605/06.
DR N-PSDB; AAZ56761.
XX
PT Proteins, polynucleotides, vectors, host cells and antibodies used to
PT diagnose, treat or prevent immune, reproductive, smooth muscle, and
PT neurological, gastrointestinal, developmental and cell proliferative
PT disorders.
XX
PS Claim 1; Page 163; 229pp; English.
XX
CC AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
CC transmembrane protein have immunospecific, antiproliferative and
CC neuroprotective activities. The human transmembrane proteins,
CC polynucleotides encoding them and other compositions and methods from the
CC present invention, can be used for the diagnosis, treatment or prevention
CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,
CC developmental and cell proliferative disorders. The HTMPN's can be used
CC to treat or prevent disorders associated with a decreased expression or
CC activity of HTMPN
XX
SQ Sequence 129 AA;
Query Match 100.0%; Score 170; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 9
AAU03498
ID AAU03498 standard; protein; 129 AA.
XX
XX AC AAU03498;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human TWEAK receptor (TWEAKR) polypeptide.
XX
KW TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;

ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
rubeosis; uveitis; macular degeneration; arthritis; rheumatism;
corneal graft neovascularisation; psoriasis; metastatic condition;
malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
preneoplastic condition; myocardial angiogenesis; wound granulation;
scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
atherosclerotic plaque neovascularisation; coronary atherosclerosis;
peripheral atherosclerosis.

Homo sapiens.

Key Location/Qualifiers
Domain 1..78
Peptide /note= "Extracellular domain"
Protein /note= "Signal peptide"
Domain 28..129
Domain 79..101
Domain /note= "Mature human TWEAKR protein"
Domain /note= "Transmembrane domain"
Domain 102..129
Domain /note= "Intracellular domain"

WO200145730-A2.

28-JUN-2001.

19-DEC-2000; 2000WO-US034755.

20-DEC-1999; 99US-0172878P.

10-MAY-2000; 2000US-0203347P.

(IMV) IMMUNEX CORP.

Wiley SR;

WPI; 2001-417975/44.

N-PSDB; RAS03963.

Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK receptor.

Example 1; Fig 1; 46pp; English.

The sequence represents the human TWEAK receptor (TWEAKR) protein. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia

Sequence 129 AA;

Query Match 100.0%; Score 170; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

Db 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

RESULT 10

ABP61512

ID ABP61512 standard; protein; 129 AA.

XX ABP61512;

AC ABP61512;

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 178.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
immunomodulator; cytosolic; antiinfective; osteopathic; nootropic;
neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-00402288.

XX 26-MAR-2001; 2001JP-00088912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ92000.

NF-approximatelykB activating gene and expressed protein, applicable in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune diseases and cancer.

Claim 4; Page 814-815; 841pp; Japanese.

The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-kB (nuclear factor kappa B) activating effect. The protein and encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition and for treating e.g. inflammations, autoimmune diseases, cancers, infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic disorders

Sequence 129 AA;

Query Match 100.0%; Score 170; DB 5; Length 129;

Best Local Similarity 100.0%; Pred. No. 3.5e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

Db 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

RESULT 11

AAU79827

ID AAU79827 standard; protein; 129 AA.

XX AAU79827;

XX 15-JUL-2002 (first entry)

XX Human type 1 transmembrane protein Fn14.

XX Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;
KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
KW tumour necrosis factor family; TNF family; TWEAK receptor;
KW myocardial ischaemic condition; myocardial infarction; wound healing;
KW burn healing; gastric ulcer; tissue transplantation;
KW organ transplantation; neovascularisation; vascular insufficiency;
KW cancer; inflammatory macular degeneration; diabetic retinopathy.
XX
OS Homo sapiens.
XX WO200222166-A2.
PN
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028451.
XX
PR 14-SEP-2000; 2000US-0232355P.
XX
XX (BIOJ) BIOGEN INC.
PA
XX Browning J, Burky L, Jakubowski A, Zheng T;
PI WPI; 2002-383103/41.
XX
XX Methods of modulating angiogenesis and inhibiting tumor progression,
PT using TWEAK receptor agonists.
PT
XX Disclosure; Fig 10A; 37pp; English.
XX
PS The invention describes methods of modulating angiogenesis and inhibiting
CC tumour progression using TWEAK (a novel member of the tumour necrosis
CC factor or TNF family) receptor agonists. Conditions which can be treated
CC using the agonists include myocardial ischaemic conditions (e.g.
CC myocardial infarction), wound healing (e.g. burn healing and healing of
CC gastric ulcers), and tissue and organ transplantations to promote
CC neovascularisation, particularly in subjects suffering from vascular
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
CC subsequently neovascularisation is useful in treatment of cancer,
CC inflammatory macular degeneration and diabetic retinopathy. This sequence
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor
CC described in the invention
XX
SQ Sequence 129 AA;
Query Match 100.0%; Score 170; DB 5; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35
RESULT 12
ID ADA56889 standard; protein; 129 AA.
XX
AC ADA56889;
XX
XX 20-NOV-2003 (first entry)
DT
XX Human secreted protein #172.
DE
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.
OS
XX WO2002102994-A2.
PN
XX 27-DEC-2002.
PD
XX 19-MAR-2002; 2002WO-US008278.
PF
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ruben SM;
PI WPI; 2003-167512/16.
XX N-PSDB; ADA55993.
DR
XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
XX Claim 13; SEQ ID NO 1079; 1754pp; English.
PS
XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 129 AA;
Query Match 100.0%; Score 170; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35
RESULT 13
ASU56716
ID ABU56716 standard; protein; 129 AA.
XX
AC ABU56716;

XX 02-APR-2003 (first entry)
XX
XX
DE Lung cancer-associated polypeptide #309.
XX
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
OS
XX WO200286443-A2.
PN
XX 31-OCT-2002.
XX
PD
XX 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
PR
PR 10-MAY-2001; 2001US-0290492P.
PR
PR 09-NOV-2001; 2001US-0339245P.
PR
PR 13-NOV-2001; 2001US-0350666P.
PR
PR 29-NOV-2001; 2001US-0334370P.
PR
PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
PI
XX WPI; 2003-0931161/08.
XX
XX N-PSDB; ABX76445.
DR
XX
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX
PS Claim 27; Page 429; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 129 AA;
Query Match 100.0%; Score 170; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVIGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVIGLWLLALLRSVAGEQAPGTAP 35
RESULT 14
ADC74112

AD74112 standard; protein; 129 AA.
ADC74112;
01-JAN-2004 (first entry)
Human secreted protein - SEQ ID 745.
antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
antidiabetic; immunosuppressive; dermatologic; nephrotropic;
antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
haemopoietic; haematologic; anaemia; autoimmune disorder;
rheumatoid arthritis; inflammation; Grave's disease; diabetes;
systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
human.
Homo sapiens.
WO2003038063-A2.
08-MAY-2003.
19-MAR-2002; 2002WO-US008277.
21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI; 2003-430516/40.
N-PSDB; ADC73497.
New human secreted polypeptide for diagnosing, preventing or treating
hematopoietic or hematologic disorders (e.g. anemia), autoimmune
disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
atherosclerosis).
Claim 16; SEQ ID NO 745; 2272pp; English.
The invention relates to a novel human secreted polypeptide comprising a
defined sequence given in the specification. The polypeptide, nucleic
acid molecule, antibody, agonist or antagonist of the invention may be
useful for preparing a composition for diagnosing or treating a
haemopoietic or haematologic disorder such as anaemia, autoimmune
disorders such as rheumatoid arthritis, inflammation, Grave's disease,
diabetes, systemic lupus erythematosus or glomerulonephritis, and
neurodegenerative disorders including Parkinson's disease and Alzheimer's
disease, wounds and hyperproliferative disorders including
atherosclerosis or cancer, as well as bacterial, viral, fungal or
parasitic infections. The polypeptide may also be used during gene
therapy procedures and for identifying a binding partner by contacting
the polypeptide with a binding partner and determining whether the
binding partner increases or decreases the activity of the polypeptide.
The current sequence is that of the human secreted protein of the
invention.
Sequence 129 AA;
Query Match 100.0%; Score 170; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRRLRLVIGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVIGLWLLALLRSVAGEQAPGTAP 35

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RESULT 15
ADD37867
ID ADD37867 standard; protein; 129 AA.
XX
AC ADD37867;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted protein #50.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
XX
OS Homo sapiens.
XX
PN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
WPI; 2003-140218/13.
DR
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 1; SEQ ID NO 349; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases, wound healing and disorders of epithelial cell
CC proliferation, immune disorders, cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein.
XX
SQ Sequence 129 AA;
Query Match 100.0%; Score 170; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRLRLRLGLWALLRSVAGEQPGTAP 35
Db 1 MARGSLRLRLRLGLWALLRSVAGEQPGTAP 35
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OM protein - protein search, using sw model

Run on: February 10, 2005, 18:17:36 ; Search time 40.6798 Seconds
(without alignments)
281.128 Million cell updates/sec

Title: US-10-062-831-59_COPY_1_35

Perfect score: 170
Sequence: 1 MARGSLRLLRLVGLMLALLRSVAGQAPCTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	112	15	US-10-351-334-139
2	170	100.0	114	14	US-10-062-831-59
3	170	100.0	114	14	US-10-062-599-59
4	170	100.0	129	9	US-09-742-454A-4
5	170	100.0	129	9	US-09-883-777-5
6	170	100.0	129	14	US-10-024-298A-178
7	170	100.0	129	14	US-10-042-211A-178
8	170	100.0	129	15	US-10-331-496A-37
9	170	100.0	129	15	US-10-295-027-444
10	170	100.0	129	15	US-10-295-027-1305
11	170	100.0	129	15	US-10-617-217A-178
12	170	100.0	155	15	US-10-351-334-284
13	170	100.0	156	15	US-10-351-334-228

14	170	100.0	300	9	US-09-883-777-9	Sequence 9, Appli
15	170	100.0	309	9	US-09-742-454A-7	Sequence 7, Appli
16	170	100.0	309	9	US-09-883-777-7	Sequence 7, Appli
17	97	57.1	129	9	US-09-742-454A-5	Sequence 5, Appli
18	97	57.1	129	9	US-09-883-777-5	Sequence 5, Appli
19	58	34.1	577	16	US-10-437-963-182042	Sequence 182042, A
20	56.5	33.2	671	15	US-10-282-122A-59634	Sequence 59634, A
21	55	32.4	465	14	US-10-156-761-13252	Sequence 13252, A
22	54.5	32.1	1120	15	US-10-262-839-6	Sequence 6, Appli
23	54.5	32.1	1188	15	US-10-291-265-338	Sequence 338, App
24	54.5	32.1	1188	15	US-10-291-265-810	Sequence 810, App
25	54.5	32.1	1189	10	US-09-984-130-35	Sequence 35, Appl
26	54.5	32.1	1189	10	US-09-836-353A-35	Sequence 35, Appl
27	54.5	32.1	1189	15	US-10-262-839-4	Sequence 4, Appli
28	54	31.8	77	9	US-09-764-860-332	Sequence 332, App
29	54	31.8	77	14	US-10-074-095-332	Sequence 332, App
30	54	31.8	77	15	US-10-212-872-332	Sequence 332, App
31	54	31.8	300	9	US-09-953-499-10	Sequence 10, Appl
32	54	31.8	300	14	US-10-265-542-10	Sequence 10, Appl
33	54	31.8	300	16	US-10-633-008-10	Sequence 10, Appl
34	54	31.8	300	16	US-10-785-220-10	Sequence 10, Appl
35	54	31.8	300	16	US-10-785-221-10	Sequence 10, Appl
36	54	31.8	300	16	US-10-785-433-10	Sequence 10, Appl
37	54	31.8	319	10	US-09-847-102A-61	Sequence 61, Appl
38	54	31.8	404	14	US-10-156-761-13020	Sequence 13020, A
39	54	31.8	647	10	US-09-847-102A-44	Sequence 44, Appl
40	54	31.8	647	14	US-10-285-976-39	Sequence 39, Appl
41	53.5	31.5	144	15	US-10-425-114-38365	Sequence 38365, A
42	53.5	31.5	159	15	US-10-425-114-48240	Sequence 48240, A
43	53.5	31.5	2098	14	US-10-132-134-36	Sequence 36, Appl
44	53	31.2	692	14	US-10-156-761-13135	Sequence 13135, A
45	53	31.2	1102	15	US-10-282-122A-67640	Sequence 67640, A

ALIGNMENTS

RESULT 1
US-10-351-334-139
; Sequence 139, Application US/10351334
; Publication No. US20040034196A1
; GENERAL INFORMATION:
; APPLICANT: Komatsoulis et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/095,454
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-334-139

Query Match 100.0%; Score 170; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;

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Qy 1 MARGSLRRLRLVGLWLLRLRSVAGEQAPGTAP 35
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Db 1 MARGSLRRLRLVGLWLLRLRSVAGEQAPGTAP 35

RESULT 2
US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match 100.0%; Score 170; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRLRSVAGEQAPGTAP 35
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Db 1 MARGSLRRLRLVGLWLLRLRSVAGEQAPGTAP 35

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match 100.0%; Score 170; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARGSLRRLRLVGLWLLRLRSVAGEQAPGTAP 35

RESULT 5
US-09-883-777-4
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Sequence 4, Application US/09883777
Patent No. US20020110853A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 129
TYPE: PRT
ORGANISM: homo sapiens
US-09-883-777-4

Query Match 100.0%; Score 170; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35
|||||

RESULT 6
US-10-024-298A-178
Sequence 178, Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAHU KASEI KABUSHIKI KAISHA
APPLICANT: Goichi HONDA
APPLICANT: Shuji MORAWATSU
APPLICANT: Yukiko NAGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: JP0088912/2001
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP402288/2000
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-298A-178

Query Match 100.0%; Score 170; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35
|||||

DB 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35

RESULT 7

US-10-042-211A-178
Sequence 178, Application US/10042211A
Publication No. US20030170719A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, Akio et al.
TITLE OF INVENTION: NFkB Activating Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/278,640
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/314,385
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match 100.0%; Score 170; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35
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DB 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35
|||||

RESULT 8

US-10-331-496A-37
Sequence 37, Application US/10331496A
Publication No. US20030228305A1
GENERAL INFORMATION:
APPLICANT: FRANTZ, GRETCHEN
APPLICANT: HILLAN, KENNETH J.
APPLICANT: PHILLIPS, HEIDI S.
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
APPLICANT: SPENCER, SUSAN D.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WU, THOMAS D.
APPLICANT: ZHANG, ZEMIN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5014R1-PCT
CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US 60/351,885
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US 60/366,284
PRIOR FILING DATE: 2002-03-21

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RESULT 11
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P

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;; CURRENT APPLICATION NUMBER: US/10/617,217A
;; CURRENT FILING DATE: 2003-07-11
;; PRIOR APPLICATION NUMBER: JP 2000-402288
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: JP 2001-088912
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: JP 2001-254018
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/258,315
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 60/278,640
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: US 60/314,385
;; PRIOR FILING DATE: 2001-08-24
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 178
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-617-217A-178

Query Match 100.0%; Score 170; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35
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Db 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35

RESULT 12
US-10-351-334-284
;; Sequence 284, Application US/10351334
;; Publication No. US20040034196A1
;; GENERAL INFORMATION:
;; APPLICANT: Komatsoulis et al
;; TITLE OF INVENTION: 98 Human Secreted Proteins
;; CURRENT APPLICATION NUMBER: US/10/351,334
;; CURRENT FILING DATE: 2003-01-27
;; PRIOR APPLICATION NUMBER: 60/350,898
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: 09/489,847
;; PRIOR FILING DATE: 2000-01-24
;; PRIOR APPLICATION NUMBER: PCT/US99/17130
;; PRIOR FILING DATE: 1999-07-29
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: 60/095,486
;; PRIOR FILING DATE: 1998-08-05
;; PRIOR APPLICATION NUMBER: 60/096,319
;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: 60/095,454
;; PRIOR FILING DATE: 1998-08-06
;; PRIOR APPLICATION NUMBER: 60/095,455
;; PRIOR FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 284
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-351-334-284

Query Match 100.0%; Score 170; DB 15; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35
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Db 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35

RESULT 13
US-10-351-334-228
;; Sequence 228, Application US/10351334
;; Publication No. US20040034196A1
;; GENERAL INFORMATION:
;; APPLICANT: Komatsoulis et al
;; TITLE OF INVENTION: 98 Human Secreted Proteins
;; FILE REFERENCE: P2031P2
;; CURRENT APPLICATION NUMBER: US/10/351,334
;; CURRENT FILING DATE: 2003-01-27
;; PRIOR APPLICATION NUMBER: 60/350,898
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: 09/489,847
;; PRIOR FILING DATE: 2000-01-24
;; PRIOR APPLICATION NUMBER: PCT/US99/17130
;; PRIOR FILING DATE: 1999-07-29
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: 60/095,486
;; PRIOR FILING DATE: 1998-08-05
;; PRIOR APPLICATION NUMBER: 60/096,319
;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: 60/095,454
;; PRIOR FILING DATE: 1998-08-06
;; PRIOR APPLICATION NUMBER: 60/095,455
;; PRIOR FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 228
;; LENGTH: 156
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; NAME/KEY: SITE
;; LOCATION: (156)
;; OTHER INFORMATION: Xaa equals stop translation
US-10-351-334-228

Query Match 100.0%; Score 170; DB 15; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35
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Db 1 MARGSLRLLRLVLLGLWLLLRVAGEQAPGTAP 35

RESULT 14
US-09-883-777-9
;; Sequence 9, Application US/09883777
;; Patent No. US20020110853A1
;; GENERAL INFORMATION:
;; APPLICANT: Wiley, Steven R.
;; TITLE OF INVENTION: TWEAK RECEPTOR
;; FILE REFERENCE: 2968-C
;; CURRENT APPLICATION NUMBER: US/09/883,777
;; CURRENT FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: US 60/172,878
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: US 60/203,347
;; PRIOR FILING DATE: 2000-05-10
;; PRIOR APPLICATION NUMBER: PCT/US00/34755
;; PRIOR FILING DATE: 2000-12-19
;; PRIOR APPLICATION NUMBER: US 09/742,454
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 300
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:

Mon Feb 14 07:22:42 2005

OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match	100.0%;	Score 170;	DB 9;	Length 300;
Best Local Similarity	100.0%;	Pred. No. 6.1e-14;		
Match	35.	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 1 MARGSLRRLRLVLTGLWALLRSVAGEQAPGTAP 35

RESULT 15

US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. US20020041876A1

; FILE# NO: 00200200-1
; GENERAL INFORMATION:

APPLICANT: WILEY, Steven R.

APPLICANT: WILEI, STEVEN R.
TITLE OF INVENTION: TWEAK RECEPTOR

; TITLE OF INVENTION: INEAK RECEPOT
; FILE REFERENCE: 2968-B

FILE REFERENCE: 2988-B
CURRENT APPLICATION NUMBER: IIS/09/742.454A

CURRENT FILING DATE: 2000-12-19
CURRENT APPLICATION NUMBER: US/00-12-19

; CURRENT FILING DATE: 2000-12-19
; PUBLICATION NUMBER: 60/172 878

; PRIOR APPLICATION NUMBER: 60/172,878
 ; FILING DATE: 1998-12-30

; PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: 60/203,347

PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

: SEO ID NO 7

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; SEQ ID NO 7
:      LENGTH: 309

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; LENGTH: 309
; TYPE: PRT
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; TYPE: PRI
OBJANTCM:

; ORGANISM: Artificial sequence

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;
FEATURE:
CURRENT INFORMATION: Description
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OTHER INFORMATION: Description of Artificial sequence: human interleukin-2

OTHER INFORMATION: receptor fusion protein construct

US-09-742-454A-7

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Query Match      100.0%; Score 170; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.3e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35 QY
1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35 db

Search completed: February 10, 2005, 18:43:36
Job time : 41.6798 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:02:18 ; Search time 14.4298 Seconds
(without alignments)
181.064 Million cell updates/sec

Title: US-10-062-831-59_COPY_1_35

Perfect score: 170
Sequence: 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	112	4	US-09-489-847-139 Sequence 139, Appl
2	170	100.0	114	4	US-09-690-454-59 Sequence 59, Appl
3	170	100.0	129	4	US-09-883-777-4 Sequence 4, Appl
4	170	100.0	129	4	US-09-883-777-4 Sequence 6914, Ap
5	170	100.0	129	4	US-09-949-016-6914 Sequence 4, Appl
6	170	100.0	155	4	US-09-742-454A-4 Sequence 284, App
7	170	100.0	156	4	US-09-489-847-284 Sequence 228, App
8	170	100.0	300	4	US-09-883-777-9 Sequence 9, Appl
9	170	100.0	309	4	US-09-883-777-7 Sequence 7, Appl
10	170	100.0	309	4	US-09-742-454A-7 Sequence 7, Appl
11	97	57.1	129	4	US-09-893-777-5 Sequence 5, Appl
12	97	57.1	129	4	US-09-742-454A-5 Sequence 5, Appl
13	54.5	32.1	1217	4	US-09-949-016-7892 Sequence 7892, Ap
14	54	31.8	300	4	US-09-254-465A-10 Sequence 10, Appl
15	54	31.8	300	4	US-09-397-243D-12 Sequence 12, Appl
16	54	31.8	300	4	US-09-953-499-10 Sequence 10, Appl
17	53	31.2	38	4	US-09-471-276-1405 Sequence 1405, Ap
18	53	31.2	48	3	US-09-453-322B-14 Sequence 14, Appl
19	52.5	30.9	680	4	US-09-489-039A-8422 Sequence 8422, Ap
20	52	30.6	108	4	US-09-513-999C-4205 Sequence 4205, Ap
21	52	30.6	518	4	US-09-893-737-84 Sequence 84, Appl
22	52	30.6	598	4	US-09-252-991A-28599 Sequence 28599, A
23	52	30.6	957	4	US-09-949-016-6154 Sequence 6154, Ap
24	52	30.6	964	4	US-09-949-016-7431 Sequence 7431, Ap
25	51.5	30.3	422	4	US-09-902-540-11389 Sequence 11389, A
26	51	30.0	148	4	US-09-489-039A-11733 Sequence 11733, A
27	50.5	29.7	156	4	US-09-902-540-12764 Sequence 12764, A

28	50.5	29.7	432	3	US-08-702-665A-3 Sequence 3, Appli
29	50.5	29.7	441	3	US-09-151-102-4 Sequence 4, Appli
30	50.5	29.7	441	3	US-08-929-846-4 Sequence 4, Appli
31	50.5	29.7	441	4	US-08-663-584-4 Sequence 4, Appli
32	50	29.4	240	4	US-09-949-016-9266 Sequence 9266, Ap
33	50	29.4	386	3	US-09-321-961-5 Sequence 5, Appli
34	50	29.4	386	4	US-09-739-861A-5 Sequence 5, Appli
35	50	29.4	386	4	US-09-795-583-5 Sequence 2, Appli
36	49	28.8	427	4	US-09-550-645-2 Sequence 2, Appli
37	49	28.8	428	4	US-09-922-364A-32 Sequence 32, Appl
38	49	28.8	428	4	US-09-254-590-32 Sequence 32, Appl
39	49	28.8	428	4	US-10-115-415-32 Sequence 32, Appl
40	49	28.8	428	4	US-10-116-260-32 Sequence 32, Appl
41	49	28.8	428	4	US-10-115-671-32 Sequence 32, Appl
42	49	28.8	510	4	US-09-949-016-10021 Sequence 10021, A
43	49	28.8	1238	3	US-09-214-278-5 Sequence 5, Appli
44	49	28.8	1238	4	US-09-855-722-5 Sequence 5, Appli
45	49	28.8	1399	3	US-08-462-467B-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match 100.0%; Score 170; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.4e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

RESULT 2
US-09-690-454-59
; Sequence 59, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144

; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59

Query Match 100.0%; Score 170; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.5e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 3
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match 100.0%; Score 170; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.7e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 4
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

Query Match 100.0%; Score 170; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.7e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 5
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match 100.0%; Score 170; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.7e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35
Db 1 MARGSLRRLRLVGLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 6
US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al

;; TITLE OF INVENTION: 98 Human Secreted Proteins
;; FILE REFERENCE: P2031P1
;; CURRENT APPLICATION NUMBER: US/09/489,847
;; EARLIER FILING DATE: 2000-01-24
;; EARLIER APPLICATION NUMBER: PCT/US99/17130
;; EARLIER FILING DATE: 1999-07-29
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; EARLIER APPLICATION NUMBER: 60/095,486
;; EARLIER FILING DATE: 1998-08-05
;; EARLIER APPLICATION NUMBER: 60/096,319
;; EARLIER FILING DATE: 1998-08-12
;; EARLIER APPLICATION NUMBER: 60/095,454
;; EARLIER FILING DATE: 1998-08-06
;; EARLIER APPLICATION NUMBER: 60/095,455
;; EARLIER FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 284
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-489-847-284

Query Match 100.0%; Score 170; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
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DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 7

US-09-489-847-228
;; Sequence 228, Application US/09489847
;; Patent No. 6476195

GENERAL INFORMATION:

;; APPLICANT: Rosen et al
;; TITLE OF INVENTION: 98 Human Secreted Proteins
;; FILE REFERENCE: P2031P1
;; CURRENT APPLICATION NUMBER: US/09/489,847
;; EARLIER FILING DATE: 2000-01-24
;; EARLIER APPLICATION NUMBER: PCT/US99/17130
;; EARLIER FILING DATE: 1999-07-29
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; EARLIER APPLICATION NUMBER: 60/095,486
;; EARLIER FILING DATE: 1998-08-05
;; EARLIER APPLICATION NUMBER: 60/096,319
;; EARLIER FILING DATE: 1998-08-12
;; EARLIER APPLICATION NUMBER: 60/095,454
;; EARLIER FILING DATE: 1998-08-06
;; EARLIER APPLICATION NUMBER: 60/095,455
;; EARLIER FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 228
;; LENGTH: 156
;; TYPE: PRT
;; ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (156)

OTHER INFORMATION: Xaa equals stop translation

US-09-489-847-228

Query Match 100.0%; Score 170; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
|||||

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 8

US-09-883-777-9

;; Sequence 9, Application US/09883777

;; Patent No. 6727225

;; GENERAL INFORMATION:

;; APPLICANT: Wiley, Steven R.

;; TITLE OF INVENTION: TWEAK RECEPTOR

;; FILE REFERENCE: 2968-C

;; CURRENT APPLICATION NUMBER: US/09/883,777

;; CURRENT FILING DATE: 2001-06-18

;; PRIOR APPLICATION NUMBER: US 60/172,878

;; PRIOR FILING DATE: 1999-12-20

;; PRIOR APPLICATION NUMBER: US 60/203,347

;; PRIOR FILING DATE: 2000-05-10

;; PRIOR APPLICATION NUMBER: PCT/US00/34755

;; PRIOR FILING DATE: 2000-12-19

;; PRIOR APPLICATION NUMBER: US 09/742,454

;; PRIOR FILING DATE: 2000-12-19

;; NUMBER OF SEQ ID NOS: 16

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 9

;; LENGTH: 300

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct

US-09-883-777-9

Query Match 100.0%; Score 170; DB 4; Length 300;

Best Local Similarity 100.0%; Pred. No. 2.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
|||||

DB 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 9

US-09-883-777-7

;; Sequence 7, Application US/09883777

;; Patent No. 6727225

;; GENERAL INFORMATION:

;; APPLICANT: Wiley, Steven R.

;; TITLE OF INVENTION: TWEAK RECEPTOR

;; FILE REFERENCE: 2968-C

;; CURRENT APPLICATION NUMBER: US/09/883,777

;; CURRENT FILING DATE: 2001-06-18

;; PRIOR APPLICATION NUMBER: US 60/172,878

;; PRIOR FILING DATE: 1999-12-20

;; PRIOR APPLICATION NUMBER: US 60/203,347

;; PRIOR FILING DATE: 2000-05-10

;; PRIOR APPLICATION NUMBER: PCT/US00/34755

;; PRIOR FILING DATE: 2000-12-19

;; PRIOR APPLICATION NUMBER: US 09/742,454

;; PRIOR FILING DATE: 2000-12-19

;; NUMBER OF SEQ ID NOS: 16

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 7

;; LENGTH: 309

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct

US-09-883-777-7

Query Match 100.0%; Score 170; DB 4; Length 309;

Best Local Similarity 100.0%; Pred. No. 2.5e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
|||||

Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 10

US-09-742-454A-7

; Sequence 7, Application US/09742454A

; Patent No. 6824773

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK Receptor

; FILE REFERENCE: 2968-B

; CURRENT APPLICATION NUMBER: US/09/742,454A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: 60/203,347

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct

US-09-742-454A-7

Query Match 100.0%; Score 170; DB 4; Length 309;

Best Local Similarity 100.0%; Pred. No. 2.5e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 11

US-09-883-777-5

; Sequence 5, Application US/09883777

; Patent No. 6727225

; GENERAL INFORMATION:

; APPLICANT: Wiley, Steven R.

; TITLE OF INVENTION: TWEAK RECEPTOR

; FILE REFERENCE: 2968-C

; CURRENT APPLICATION NUMBER: US/09/883,777

; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 60/203,347

; PRIOR FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: PCT/US00/34755

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/742,454

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-883-777-5

Query Match

Best Local Similarity 57.1%; Score 97; DB 4; Length 129;

Matches 21; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 12

US-09-742-454A-5

; Sequence 5, Application US/09742454A

; Patent No. 6824773

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK Receptor

; FILE REFERENCE: 2968-B

; CURRENT APPLICATION NUMBER: US/09/742,454A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: 60/203,347

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-742-454A-5

Query Match 57.1%; Score 97; DB 4; Length 129;

Best Local Similarity 60.0%; Pred. No. 2.5e-06;

Matches 21; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35
|||||

RESULT 13

US-09-949-016-7892

; Sequence 7892, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C0001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7892

; LENGTH: 1217

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7892

Query Match

Best Local Similarity 32.1%; Score 54.5; DB 4; Length 1217;

Matches 14; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

Qy 9 LLRLVLGLW-LALLRSVAGEQAPGTAP 35
|||||Db 1184 LLALLVLLMWKLGPFRRSRRRRRRLGLDP 1211
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RESULT 14

US-09-254-465A-10

; Sequence 10, Application US/09254465A

; Patent No. 6410708

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Fong, Sherman

```

; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 10
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-254-465A-10

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Query Match 31.8%; Score 54; DB 4; Length 300;
Best Local Similarity 44.4%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

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QY 9 LRLVLGLWLLRSVAGEQAPGTAP 35
|||:|:|:|:|
DB 249 LIGLLIFGVWFAYSRGYFETTKGTAP 275

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RESULT 15
US-09-397-243D-12
; Sequence 12, Application US/09397243D
; Patent No. 6699688
; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; PRIOR FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-397-243D-12

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```

Query Match 31.8%; Score 54; DB 4; Length 300;
Best Local Similarity 44.4%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

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QY 9 LRLVLGLWLLRSVAGEQAPGTAP 35
|||:|:|:|:|
DB 249 LIGLLIFGVWFAYSRGYFETTKGTAP 275

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Search completed: February 10, 2005, 18:18:45
Job time : 15.4298 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	64	31.5	261	2	G69099	probable pyruvate
2	63.5	31.3	893	2	S51603	receptor-like tyro
3	63.5	31.3	898	2	S47489	receptor tyrosine
4	63.5	31.3	981	2	S51604	receptor-like tyro
5	63.5	31.3	1005	2	S49015	receptor tyrosine
6	61	30.0	390	2	F69086	pyruvate formate-1
7	60.5	29.8	76	2	T03860	TA20 protein - com
8	59.5	29.3	414	2	T15947	hypothetical prote
9	59.5	29.3	431	1	B69092	conserved hydrop
10	59.5	29.3	1013	2	I50615	receptor-type prot
11	59.5	29.3	1210	1	Q8HUE	epidermal growth f
12	59	29.1	55	1	FEPE	ferredoxin 2[4Fe--
13	58.5	28.8	1210	2	A53183	epidermal growth f
14	58.5	28.8	1548	2	S34583	serine proteinase
15	58	28.6	197	2	T50025	hypothetical prote
16	57.5	28.3	644	2	A36325	epidermal growth f
17	56	27.6	103	2	T08775	hypothetical prote
18	56	27.6	2871	2	A55624	fibrillin-1 precur
19	55.5	27.3	59	1	FEDV2N	ferredoxin 2[4Fe--
20	55.5	27.3	991	1	T18843	receptor protein-t
21	54.5	26.8	464	2	S48329	probable membrane
22	54.5	26.8	560	2	T16833	hypothetical prote
23	54.5	26.8	932	2	I52524	PAC5A - mouse (fr
24	54	26.6	421	1	HQDVLV	cytochrome-c3 hvd
25	53.5	26.4	97	2	AB2120	ferredoxin [import
26	53.5	26.4	281	2	H84263	chloromonas cyc
27	53	26.1	63	2	C69303	ferredoxin (fdx-4)
28	53	26.1	286	2	T49505	hypothetical prote
29	53	26.1	319	2	E84528	hypothetical prote

RESULT 5
S49015
receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)

```

RESULT 7
T03860
TA20 protein - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T03860
R/Beals, T.P.; Goldberg, R.B.
submitted to the EMBL Data Library, October 1996
A/Description: Nicotiana tabacum gene expressed in anther.
A/Reference number: Z15122

```


A:Cross-references: GB:M11234; NID:g181981; PIDN:AA52370.1; PID:g553272
R:Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ulrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A:Title: The human EGF receptor gene: structure of the 110 kb locus and identification of
A:Reference number: S30024; MUID:88217333; PMID:3329716
A:Accession: S30024
A:Molecule type: DNA
A:Residues: 1-29 <HA2>
A:Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R:Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A:Title: Contributory effects of de Novo transcription and premature transcript termination
A:Reference number: A38672; MUID:91107677; PMID:1988448
A:Accession: A38672
A:Molecule type: DNA
A:Residues: 1-29 <HAL>
A:Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A:Experimental source: carcinoma cell line A431-7
R:Xu, Y.; Tahli, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Mead
Nature 309, 806-810, 1984
A:Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs
A:Reference number: A00642; MUID:84245835; PMID:6330563
A:Accession: A00642
A:Molecule type: mRNA
A:Residues: 'RCAWERRA', 150-187, 'KSVIOAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321
, 798-799, 'TD', 802-811, 'R', 813-942 <XUY>
A:Experimental source: A431 human carcinoma cells, which have large numbers of EGF receptor
R:Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.
Science 224, 843-848, 1984
A:Title: Expression cloning of human EGF receptor complementary DNA: gene amplification
A:Reference number: A43615; MUID:84196372; PMID:6326261
A:Accession: A43615
A:Molecule type: mRNA
A:Residues: 713-964 <LIN>
A:Experimental source: epidermoid carcinoma cell line A431
R:Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A:Reference number: A23062; MUID:85046483; PMID:6093780
A:Accession: A23062
A:Molecule type: mRNA
A:Residues: 1028-1210 <SIM>
R:Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A:Reference number: A05281; MUID:84172183; PMID:6324343
A:Accession: A05281
A:Molecule type: protein
A:Residues: 25-30, 'S', 32-51, 454-467 <WEB>
R:Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A:Title: Identification of residues in the nucleotide binding site of the epidermal growth
A:Reference number: A60143; MUID:85182650; PMID:2985580
A:Accession: A60143
A:Molecule type: protein
A:Residues: 740-744, 'X', 746-747 <RUS>
R:Mróczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A:Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide
A:Reference number: A38023; MUID:84191554; PMID:6325948
A:Contents: annotation; receptor activity
A:Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R:Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
Cell 59, 33-43, 1989
A:Title: Functional independence of the epidermal growth factor receptor from a domain 2
A:Reference number: A3331; MUID:90003233; PMID:2790960
A:Contents: annotation; internalization signal
A:Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex
C:Genetics:
A:Gene: GDB:EGFR
A:Cross-references: GDB:120610; OMIM:131550
A:Map position: 7p12.3-7p12.1
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1210/Product: EGF receptor #status predicted <MAT>
F:25-645/Domain: extracellular #status predicted <EXT>
F:75-300/Domain: EGF receptor extracellular domain repeat <BE1>
F:390-600/Domain: EGF receptor extracellular domain repeat <BE2>
F:646-668/Domain: transmembrane #status predicted <TMW>
F:669-1210/Domain: intracellular #status predicted <INT>
F:710-975/Domain: protein kinase homology <KIN>
F:718-726/Region: protein kinase ATP-binding motif
F:999-1046/Region: coated-pit mediated internalization signal
F:1047-1210/Region: inhibitory
F:128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:745/Active site: Lys #status experimental

Query Match 29.3%; Score 59.5; DB 1; Length 1210;
Best Local Similarity 35.6%; Pred. No. 18; Indels 11; Gaps 3;
Matches 16; Conservative 2; Mismatches 16

Qy 1 CSRGSSWSADLDKCMD-----CAS-----CRARPHSDFCLG-CAA 34
Db 194 CPNGSGWAGBENCQKLTIKICQAQCSGRCGRKSPDCCHNQCAA 238

RESULT 12

FEPE
A:Title: ferredoxin 2[4Fe-4S] [validated] - Peptostreptococcus asaccharolyticus
C:Species: Peptostreptococcus asaccharolyticus
C:Date: 24-Apr-1984 #sequence_revision 23-Mar-1995 #text_change 12-Jul-2004
C:Accession: A00196
R:Tsunoda, J.N.; Yasunobu, K.T.; Whiteley, H.R.
J. Biol. Chem. 243, 6262-6272, 1968
A:Title: Non-heme iron proteins. IX. The amino acid sequence of ferredoxin from Micrococcus
A:Reference number: A92040; MUID:69054261; PMID:5723466
A:Note: the source is designated as Micrococcus aerogenes
A:Accession: A00196
A:Molecule type: protein
A:Residues: 1-21,23-24,'Q',26-55 <TSU>
A:Cross-references: UNIPROT:P00193
R:Backes, G.; Mino, Y.; Loehr, T.M.; Meyer, T.E.; Cusanovich, M.A.; Sweeney, W.V.; Adman
J. Am. Chem. Soc. 113, 2055-2064, 1991
A:Title: The environment of Fe4S4 clusters in ferredoxins and high-potential iron proteins
A:Reference number: A44688
A:Contents: annotation; X-ray crystallography, 2.0 angstroms; sequence revision
A:Note: sequence correction confirmed by peptide sequencing
R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.
submitted to the Brookhaven protein data bank, August 1976
A:Reference number: A50836; PDB:1FDX
R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.
J. Biol. Chem. 251, 3801-3806, 1976
A:Title: Structure of Peptococcus aerogenes ferredoxin. Refinement at 2 angstroms resolution
A:Reference number: A92192; MUID:76213238; PMID:932007
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.
J. Biol. Chem. 248, 3987-3996, 1973
A:Title: The structure of a bacterial ferredoxin.
A:Reference number: A92136; MUID:73187389; PMID:4708097
A:Contents: annotation; X-ray crystallography, 2.8 angstroms
C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
F:1-54/Domain: ferredoxin 2[4Fe-4S] homology <FER>
F:8,11,14,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental
F:18,36,39,42/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 29.1%; Score 59; DB 1; Length 55;
Best Local Similarity 52.9%; Pred. No. 2.1; Indels 5; Gaps 0;
Matches 9; Conservative 3; Mismatches 5

Qy 4 GSSWSADLDKCMDASC 20
Db 26 GSIYVADADSCIDGSC 42

RESULT 13

A53183

epidermal growth factor receptor precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C:Accession: A53183; S24942; A28941; S45325; I49643
R:Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;
Genes Dev. 8, 399-413, 1994
A:Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor
A:Reference number: A53183; MUID:94170986; PMID:8125255
A:Accession: A53183
A:Molecule type: mRNA
A:Residues: 1-1210 <LUE>
A:Cross-references: UNIPROT:Q01279; GB:U03425
R:Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.
Oncogene 6, 673-676, 1991
A:Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site
A:Reference number: A43818; MUID:91232866; PMID:2030916
A:Accession: A43818
A:Molecule type: mRNA
A:Residues: 1-714 <AVI>
A:Cross-references: GB:X59698
R:Eisinger, D.P.; Serrero, G.
submitted to the EMBL Data Library, June 1992
A:Reference number: S24942
A:Accession: S24942
A:Molecule type: mRNA
A:Residues: 969-971, 'K', 973-1115, 'D' <BIS>
A:Cross-references: EMBL:Z12608
R:Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A:Title: Epidermal growth factor receptor threonine and serine residues phosphorylated
A:Reference number: A28941; MUID:88330814; PMID:3138233
A:Accession: A28941
A:Molecule type: protein
A:Residues: 689-694, 'X', 696-704, 'L', 706-707, 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1009,
R:Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A:Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
A:Reference number: S45325
A:Accession: S45325
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-971, 'K', 973-1210 <VER>
A:Cross-references: EMBL:X78987; NID:9488830; PIDN:CAA55587.1; PID:9488831
R:Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A:Title: Expression of the epidermal growth factor receptor gene is regulated in mouse
A:Reference number: I49643; MUID:93126380; PMID:7678348
A:Accession: I49643
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 12-20, 22-132 <RES>
A:Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
C:Genetics:
A:Gene: EGFR
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphoprotein
P:1-24/Domain: signal sequence #status predicted <SIG>
P:648-670/Domain: transmembrane #status predicted <TM>
P:712-977/Domain: protein kinase homology <KIN>
P:720-728/Region: protein kinase ATP-binding motif
P:680,695/Binding site: phosphate (Thr) (covalent) #status experimental
P:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
P:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
P:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
P:1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 28.8%; Score 58.5; DB 2; Length 1210;
Best Local Similarity 35.6%; Pred. No. 24;
Matches 16; Conservative 1; Mismatches 17; Indels 11; Gaps 3;

QY 1 CSRGSSWADLDKCMD-----CAS-----CRPHSDPCLG-CAA 34

DB 194 CPNGSCWGGGENCKLTKIIICAAQCCHRCGRSPSCDCHNQCAA 238

RESULT 14

S34583

serine proteinase (EC 3.4.21.-) PC68 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S34583

R:Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993

A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a

A:Reference number: S34583; MUID:93327934; PMID:8335106

A:Accession: S34583

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1548 <NAK>

A:Cross-references: UNIPROT:Q04592; GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:dl100503

C:Keywords: hydrolase; serine proteinase

Query Match 28.8%; Score 58.5; DB 2; Length 1548;

Best Local Similarity 40.0%; Pred. No. 28;

Matches 14; Conservative 3; Mismatches 15; Indels 3; Gaps 2;

QY 1 CSRGSSWADLDKCMD-ASCRA--RPHSDPCLGC 32

DB 1201 CPEGYHTDKSQCVLCHSSCRCEGPHSMQCLSC 1235

RESULT 15

T50025

hypothetical protein T31P16.200 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T50025

R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Kalicki, J.; Wohlmann, P.; S.

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25027

A:Accession: T50025

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-197 <BEV>

A:Cross-references: UNIPROT:Q9LX09; EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.200

A:Experimental source: cultivar Columbia; BAC clone T31P16

C:Genetics:

A:Gene: ATSP:T31P16.200

A:Map position: 5

C:Superfamily: Arabidopsis thaliana hypothetical protein T31P16.200

Query Match 28.6%; Score 56; DB 2; Length 197;

Best Local Similarity 38.5%; Pred. No. 7.1;

Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 10 DLDKCMDASCARPHSDPCLGCAAA 35

DB 170 DLCECKDRCNCVDYEAFFVACALA 195

Search completed: February 10, 2005, 18:20:12

Job time : 12.2851 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 18:01:53 ; Search time 50.1974 seconds
(without alignments)
357.046 Million cell updates/sec

Title: US-10-062-831-59_COPY_36_70

Perfect score: 203

Sequence: 1 CSRGSWSADLDKCMDCASCRPHSDPCLGCAAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203	100.0	129	1 FN14 HUMAN	Q9np84 homo sapien
2	190	93.6	129	1 FN14 MOUSE	Q9cr75 m tumor nec
3	190	93.6	129	2 Q80X9	Q80x9 rattus norv
4	95	46.8	120	2 Q8SIX7	Q8six7 xenopus lae
5	64	31.5	81	1 PORD METH	P56815 methanobact
6	63.5	31.3	420	2 Q8CBY9	Q8cb99 mus musculu
7	63.5	31.3	538	2 Q8C278	Q8c278 mus musculu
8	63.5	31.3	681	2 Q8C276	Q8c276 mus musculu
9	63.5	31.3	1005	1 EPAS RAT	P54757 rattus norv
10	62.5	30.8	1209	2 Q8MIL8	Q8mil8 sus scrofa
11	61	30.0	56	2 Q7MUS0	Q7mus0 porphyronon
12	61	30.0	390	2 Q27680	O27680 methanobact
13	60.5	29.8	76	2 Q24155	O24155 nicotiana t
14	60.5	29.8	191	2 Q7Q0R6	Q7q0r6 giardia lam
15	60.5	29.8	495	1 MLP2 DROME	Q24400 drosophila
16	60.5	29.8	1615	2 Q7QZU9	Q7qzu9 giardia lam
17	60	29.6	54	1 FER PEPAS	P00193 peptostrept
18	59.5	29.3	414	2 Q19088	Q8tfs5 pyrobaculum
19	59.5	29.3	414	2 Q19088	Q19088 caenorhabdi
20	59.5	29.3	431	1 YG84 METH	O27719 methanobact
21	59.5	29.3	645	2 Q8G8S6	Q8g8s6 homo sapien
22	59.5	29.3	1013	1 EPAS CHICK	P54755 gallus gall
23	59.5	29.3	1210	1 EGFR HUMAN	P00533 homo sapien
24	58.5	28.8	328	2 Q76B98	Q76b98 xenopus lae
25	58.5	28.8	396	2 Q7T316	Q7t316 brachydanio
26	58.5	28.8	420	2 P91776	P91776 pacifastacu
27	58.5	28.8	478	2 Q8ESE0	Q8ese0 rattus norv
28	58.5	28.8	643	2 Q8ERV6	Q8erv6 mus musculu
29	58.5	28.8	645	2 Q6NPA0	Q6npa0 drosophila
30	58.5	28.8	655	2 Q9WVF5	Q9wvf5 m epidermal
31	58.5	28.8	751	2 Q9VTR2	Q9vtr2 drosophila

32	58.5	28.8	1210	1 EGFR MOUSE	Q01279 mus musculu
33	58.5	28.8	1210	2 Q9EP98	Q9ep98 mus musculu
34	58.5	28.8	1877	1 PKC5 MOUSE	Q04592 mus musculu
35	58	28.6	197	2 Q9LX09	Q9lx09 arabidopsis
36	58	28.6	291	2 Q749U7	Q749u7 geobacter s
37	58	28.6	343	2 Q67JAS	Q67jas symbiobacte
38	58	28.6	789	2 Q8N1E9	Q8n1e9 homo sapien
39	58	28.6	1340	2 Q7PHU6	Q7phu6 anopheles g
40	58	28.6	1429	2 Q7PBN5	Q7pbn5 anopheles g
41	58	28.6	1433	2 Q9BIH9	Q9bih9 anopheles g
42	58	28.6	2291	2 Q9WIA9	Q9wia9 drosophila
43	57.5	28.3	782	2 Q963D5	Q963ds apis mellif
44	57.5	28.3	1209	2 Q9QX70	Q9qx70 rattus norv
45	57.5	28.3	1696	1 PKC5_BACL	Q9nj15 branchiosto

ALIGNMENTS

RESULT 1
FN14_HUMAN
ID FN14_HUMAN STANDARD; PRT; 129 AA.
AC Q9NP84; Q9HCS0;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member Fn14 precursor
DE (Fibroblast growth factor receptor-inducible early response protein
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).
GN Name=TNFRSF12A; Synonyms=FN14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=20216634; PubMed=10751351;
RA Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,
RA Testa J.R., Feifley K.A., Winkles J.A.;
RT "The Fn14 immediate-early response gene is induced during liver
RT regeneration and highly expressed in both human and murine
RT hepatocellular carcinomas";
RL Am J. Pathol. 156:1253-1261(2000).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Tanaka S., Sugimachi K.;
RL "Human homologue of Fn14";
RP Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Uterus;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).


```

RN  [4]
RP  FUNCTION.
RX  MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;
RA  Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RT  Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RT  "A novel TNF receptor family member binds TWEAK and is implicated in
RT  angiogenesis.";
RL  Immunity 15:837-846(2001).
CC  -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC  some cell types. Promotes angiogenesis and the proliferation of
CC  endothelial cells. May modulate cellular adhesion to matrix
CC  proteins.
CC  -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC  TRAF3.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1;
CC  IsoId=Q9NP84-1; Sequence=Displayed;
CC  Name=2;
CC  IsoId=Q9NP84-2; Sequence=VSP_006519;
CC  -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC  kidney. Intermediate expression in lung, skeletal muscle and
CC  pancreas.
CC  -!- INDUCTION: By FGF-1 and phorbol ester.
CC  -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF191148; BAA69108.1; -
DR  EMBL; AB035480; AAF94792.1; -
DR  EMBL; AB035481; BAB17850.1; -
DR  EMBL; BC002718; AAO2718.1; -
DR  EMBL; GenBank; HGNC:18152; TNFSF12A.
DR  H-InvDB; HIX0012751; -
DR  MIM; 605914; -
DR  GO; GO:0006928; P:cell motility; TAS.
DR  GO; GO:0007275; P:development; TAS.
DR  InterPro; IPR001368; TNFR_c6.
DR  PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR  PROSITE; PS00050; TNFR_NGFR_2; FALSE NEG.
KW  Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;
KW  Receptor; Signal; Transmembrane.
FT  SIGNAL 1 27 Potential.
FT  CHAIN 28 129 Tumor necrosis factor receptor
FT  superfamily member Fn14.
FT  DOMAIN 28 80 Extracellular (Potential).
FT  TRANSMEM 81 101 Potential.
FT  DOMAIN 102 129 Cytoplasmic (Potential).
FT  REPEAT 36 67 TNFR-Cys (atypical).
FT  DISULFID 36 49 Potential.
FT  DISULFID 52 67 Potential.
FT  VARSPLIC 33 67 Missing (in isoform 2).
FT  /FTid=VSP_006519.
SQ  SEQUENCE 129 AA; 13911 MW; BF3FDFB9C1E1C448 CRC64;
Query Match 100.08; Score 203; DB 1; Length 129;
Best Local Similarity 100.08; Pred. No. 8e-18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSRSSGSADLDKCMDCASCARPHSDFCLGCAA 35
Db 36 CSRSSGSADLDKCMDCASCARPHSDFCLGCAA 70
RESULT 2
FN14_MOUSE

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ID  FN14_MOUSE STANDARD; PRT; 129 AA.
AC  Q9CR75; Q9QZK3;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Tumor necrosis factor receptor superfamily member Fn14 precursor
DE  (Fibroblast growth factor-inducible immediate-early response protein
DE  14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)
DE  (Weak-receptor) (TweakR).
DE  Name=TNFSF12a; Synonyms=Fgfrp2, Fn14;
GN  Mus musculus (Mouse)
OS  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c; TISSUE=Fibroblast;
RC  MEDLINE=20020297; PubMed=10551889; DOI=10.1074/jbc.274.46.33166;
RX  Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,
RA  Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA  Richards C.M., Winkles J.A.;
RA  "The mitogen-inducible Fn14 gene encodes a type I transmembrane
RT  protein that modulates fibroblast adhesion and migration.";
RL  J. Biol. Chem. 274:33166-33176(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;
RX  MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
RA  Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA  Nikaide I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA  Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA  Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA  Schriber L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA  Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA  Dalla E., Dragani T.A., Fietcher C.F., Forrest A., Frazer K.S.,
RA  Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA  Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA  Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA  Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA  Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA  Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA  Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA  Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA  Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M.,
RA  Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RA  Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA  Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA  Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA  Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA  Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA  Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA  Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA  Yasunishi A., Yoshino M., Waterston K., Lander E.S., Rogers J.,
RA  Birney E., Hayashizaki Y.;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Breast tumor;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
RA  Brownstein M.J., Uscin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.H.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RL Mueller A.M., Giegerich G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TTSUVE=pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettanan M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RP SEQUENCE FROM N.A.
RC TTSUVE=pituitary gland;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR ENBL; AY255102; AAP06753.1; -.
DR ENBL; BC060537; RAH60537.1; -.
DR GO; GO:0016021, C:integral to membrane, IEA.
DR InterPro; IPR002212; Fibрил-asoc.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match 93.6%; Score 190; DB 2; Length 129;
Best Local Similarity 94.3%; Pred. No. 3,4e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 1 CSRGSSWSADLKCNDCAACSCAPRHPSDFCLGCAA 35
Db 36 CSRGSSWSADLKCNDCAACSCAPRHPSDFCLGCAA 70

RESULT 4
ID Q6SIX7 PRELIMINARY; PRT; 120 AA.
AC Q6SIX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnl4.
OS Xenopus laevis (African clawed frog).
GN Xenopus laevis
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RC TTSUVE=Heart;
RA Brown S.A.N., Winkles J.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR ENBL; AY458020; AAR21225.1; -.

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SQ SEQUENCE 120 AA; 13295 MW; F5B5D0BBA3F7B4F CRC64;
Query Match 46.8%; Score 95; DB 2; Length 120;
Best Local Similarity 46.9%; Pred. No. 0.00027;
Matches 15; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CSRGSSVADLDKCMDCASCRCARHPDFCLGC 32
   |||||
Db 27 CPFGAYSQDLGKCMCEVCNKSFKSCQNC 58

RESULT 5
PORD METHTH STANDARD; PRT; 81 AA.
AC P56815;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
GN Name=pord; OrderedLocNames=WHI740.1;
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Ji Wani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RA "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -|- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -|- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
CC -|- CAUTION: There seems to be a sequencing error that fuses together
CC pord and pord. We have cut the ORF into its two constituents.
-----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AE000929; AAB86210.1; ALT_INIT.
DR HSPF; P00195; ICBF.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4SFRDXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Complete proteome; Electron transport; Iron-sulfur;
KW Oxidoreductase; Repeat.
FT METAL 34 34 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 37 37 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 40 40 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 44 44 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 60 60 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 63 63 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 66 66 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 70 70 Iron-sulfur 1 (4Fe-4S) (Potential).
SQ SEQUENCE 81 AA; 9121 MW; 219A9CCA8A41604 CRC64;
```

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Query Match 31.5%; Score 64; DB 1; Length 81;
Best Local Similarity 31.9%; Pred. No. 1.4;
Matches 15; Conservative 5; Mismatches 11; Indels 16; Gaps 3;

Qy 2 SRGSSWSA-----DLDKMDCASCRA-----RPHS-----DFCLGC 32
   |||||
Db 17 NKTGSWTFKPVLDKDKCIDCDNCILFCPEGCINREHIDYDYCKGC 63

RESULT 6
Q8CBY9 PRELIMINARY; PRT; 420 AA.
AC Q8CBY9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched
DE library, clone:9330174B07 product:Eph receptor A5, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
```

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AK034289; BAC28660.1; -;
DR HSSP; P54763; 1NUK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001426; Ykase_receptor.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR ProDom; PD001495; Ephrin receptor; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
KW Receptor.
SQ SEQUENCE 420 AA; 46434 MW; 8860ADE8F73C98D4 CRC64;

Query Match 31.3%; Score 63.5; DB 2; Length 420;
Best Local Similarity 31.9%; Pred.No. 7.5; Mismatches 16; Indels 15; Gaps 2;
Matches 15; Conservative 1; 1

QY 1 CSRSWSADLDKCM-----DCASCR-----ARPHSDFCLGC 32
DB 278 CSAEGELVPIGCKMCKAGYEKNGTCQCRGFFKASPHSQTCSKC 324

RESULT 7
Q8C278 PRELIMINARY; PRT; 538 AA.
AC Q8C278;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:E530011F10 product:Eph receptor A5, full
DE insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Carninci P., Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi I., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AK089130; BAC40761.1; -;
DR HSSP; P54763; 1NUK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001426; Ykase_receptor.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 1.
DR PRINTS; PR00014; FNTVPEIII.
DR ProDom; PD001495; Ephrin receptor; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
KW Receptor.
SQ SEQUENCE 538 AA; 59823 MW; CF48C4F981452515 CRC64;

Query Match

31.3%; Score 63.5; DB 2; Length 538;

RA Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
 RA Lasmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
 RT receptor tyrosine kinase in brain.";
 RL Neuroscience 63:163-178(1994)
 CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC IsoId=P54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoId=P54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
 CC Name=5;
 CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
 CC Name=6;
 CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
 CC -!- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system. Predominantly expressed in neurons.
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC -----
 DR EMBL; X78589; CAA55357.1; -;
 DR PIR; S49015; S49015;
 DR PIR; S51603; S51603;
 DR HSP; P54763; IJFA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003962; FnIII_subd.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRODOM; P00109; TYRKINASE.
 DR PRODOM; P001495; Ephrin_receptor; 1.
 DR PRODOM; P000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS01186; EGF_2;
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KW ALTERNATIVE SPLICING; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 1005 Ephrin type-A receptor 5.
 FT DOMAIN 27 575 Extracellular (Potential).
 FT TRANSMEM 576 596 Potential.
 FT DOMAIN 597 1005 Cytoplasmic (Potential).
 FT DOMAIN 222 356 Cys-rich.
 FT DOMAIN 359 461 Fibronectin type-III 1.
 FT DOMAIN 471 561 Fibronectin type-III 2.
 FT DOMAIN 677 938 Protein kinase.
 FT DOMAIN 967 1005 SAM.
 FT NP_BIND 683 691 ATP (By similarity).
 FT BINDING 709 709 ATP (By similarity).
 FT ACT_SITE 802 802 By similarity.
 FT MOD_RES 652 652 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 658 658 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 984 984 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 10 20 GRRRTQGRGGG -> DADGPRQAQSMWCHARR (in
 FT isoform 6).
 FT FTID=VSP_003000.
 FT VARSPLIC 306 357 VCRPGFFKASPHSQTCKSCPPHSYTHEASVSCVCEKDYFR
 FT RESDPPPTMACT -> G (in isoform 2 and
 FT isoform 5).
 FT FTID=VSP_003001.
 FT VARSPLIC 358 470 RPPSAPRNAISNNVETSVFLEWIPADTGGGKQVSYIILCK
 FT KCSHAGVCEGSGHVRYPQOIGKNTSVMMADPLAHINY
 FT TFEIEAVNGVSDSPGTRQYVNVNTNOAA -> T (in
 FT isoform 3, isoform 4, isoform 5 and
 FT isoform 6).
 FT FTID=VSP_003002.
 FT VARSPLIC 597 621 SGSCCEGCGRASSLCVAHPSLIW -> R (in
 FT isoform 4 and isoform 5).
 FT FTID=VSP_003003.
 FT CONFLICT 170 170 D -> E (in Ref. 2).
 FT CONFLICT 566 566 G -> A (in Ref. 2).
 FT CONFLICT 578 578 G -> A (in Ref. 2).
 FT CONFLICT 669 669 G -> A (in Ref. 2).
 FT CONFLICT 708 708 T -> I (in Ref. 2).
 FT CONFLICT 979 979 T -> I (in Ref. 2).
 SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
 Query Match 31.3%; Score 63.5; DB 1; Length 1005;
 Best Local Similarity 31.9%; Pred. No. 17;
 Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;
 Oy 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGC 32
 ||| :|||
 Db 278 CSARGEMLVPIGKCMCKAGYEKNGTCQVCRPGFFKASPHSQTCKC 324
 ||| :|||
 RESULT 10;
 Q8MIL8;
 ID Q8MIL8 PRELIMINARY; .PRT; 1209 AA.
 AC Q8MIL8;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
 DE Epidermal growth factor receptor.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY117054; AAM77472.1; -.
 DR HSSP; Q9H2C9; 1M17.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
 DR InterPro; IPR000345; CyC heme_BS.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow fac recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0261; FU; 5.
 DR SMART; SMO0219; TyrRC; 1.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1209 AA; 133531 MW; 268E3F811E36F90F CRC64;

Query Match 30.8%; Score 62.5; DB 2; Length 1209;
 Best Local Similarity 37.8%; Pred. No. 27;
 Matches 17; Conservative 1; Mismatches 16; Indels 11; Gaps 3;

Qy 1 CSRGSSWADLDKCMD-----CAS-----CRAPHSDFCLG-CAA 34
 Db 134 CLNGSCWGAGKENCOKLTKVICAQCRCGRSPSCCHNQCAA 238

RESULT 11
 ID Q7MUS0 PRELIMINARY; PRT; 56 AA.
 AC Q7MUS0;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Periredoxin, 4Fe-4S
 GN OrderedLocNames=PGI421;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL; AE017176; AAQ66475.1; -.
 DR HSSP; P00195; ICLF.
 DR TIGR; PGI421; -.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR000813; 7Fe_ferredoxin.
 DR Pfam; PF00037; Fer4; 2.
 DR PRINTS; PR00353; 4FE4SFRDOXIN.
 DR PRINTS; PR00354; 7FE8SFRDOXIN.
 DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
 KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 56 AA; 5688 MW; 571153F92BB10C57 CRC64;

Query Match 30.0%; Score 61; DB 2; Length 56;
 Best Local Similarity 47.6%; Pred. No. 2;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 SRGSSWADLDKCMDCASCEA 22
 Db 25 SEGSYKIDATCTIDCGTCAA 45

RESULT 12
 ID O27680 PRELIMINARY; PRT; 390 AA.
 AC O27680;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Pyruvate formate-lyase activating enzyme related protein.
 GN OrderedLocNames=WH1643;
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AE000923; AAB86116.1; -.
 DR PIR; F69086; F69086.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR006638; Elp3/Miab/NifB.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR007197; Radical_SAM.
 DR Pfam; PF00037; Fer4; 1.
 DR Pfam; PF04055; Radical SAM; 1.
 DR PRINTS; PR00353; 4FE4SFRDOXIN.
 DR SMART; SM00729; Elp3; 1.
 KW PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Lyase; Metal-binding; Pyruvate.
 SQ SEQUENCE 390 AA; 42559 MW; B1F207E290AD52FC CRC64;

Query Match 30.0%; Score 61; DB 2; Length 390;
 Best Local Similarity 43.5%; Pred. No. 14;

Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 12 DKMDCASCARPHSDFCIGCAA 34
 Db 14 DRCGCGNCKSENCTGCGA 36

RESULT 13

Q24155 PRELIMINARY; PRT; 76 AA.
 AC Q24155;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE TA20 protein.
 GN Name=TA20;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Anther;
 RA Beals T.P., Goldberg R.B.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U73164; AAB18190.1; -;
 DR PIR; T03860; T03860.
 DR InterPro; IPRO01212; Somatomedin_B.
 DR PRINTS; PR00022; SOMATOMEDINB.
 SQ SEQUENCE 76 AA; 8269 MW; 2F0A47BF7A52F7CC CRC64;

Query Match 29.8%; Score 60.5; DB 2; Length 76;

Best Local Similarity 40.0%; Pred. No. 3.7; Indels 5; Gaps 1;

QY 5 SWSADLDKCMD-----CASCARPHSDFC 29

Db 27 SSYAADGSDCTDHCAITCAFCNGKQYNVC 56

RESULT 14

Q7QOR6 PRELIMINARY; PRT; 191 AA.
 AC Q7QOR6;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE GLP 24.24180.23605.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G.;
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AACB01000143; EAA37372.1; -;
 DR HSSP; P01180; 1JK6.
 DR InterPro; IPRO06058; 2Fe2S_fd_BS.
 DR InterPro; IPRO009030; Grow_fac_recpt.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
 SQ SEQUENCE 191 AA; 18964 MW; 8F52AED18A477E5B CRC64;

Query Match 29.8%; Score 60.5; DB 2; Length 191;

Best Local Similarity 41.2%; Pred. No. 8.7;

Matches 14; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 1 CSRGSSWADLDKCMDCAS-CRARPHSDFCIGCAA 33
 Db 46 CKRG--WHLAGDCLACSPCAACSSAASCLACA 77

RESULT 15

MLP2 DROME
 ID MLP2 DROME STANDARD; PRT; 495 AA.
 AC Q24400; Q3VI62;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Muscle LIM protein Mlp84B.
 GN Name=Mlp84B; Synonyms=LIM3; ORFNames=CG10699;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, TISSUE
 SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=96387325; PubMed=8794860; DOI=10.1083/jcb.134.5.1179;
 RT Stronach B.E., Siegrist S.E., Beckerle M.C.;
 RT "Two muscle-specific LIM proteins in Drosophila.";
 RL J. Cell Biol. 134:1179-1195(1996).
 RN [2]
 RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=99328429; PubMed=10397768;
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;
 RT "Muscle LIM proteins are associated with muscle sarcomeres and require
 DMEF2 for their expression during Drosophila myogenesis.";
 RL Mol. Biol. Cell 10:2329-2342(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balleson R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasearman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.;"
RL Science 287:2185-2195(2000).
RN [4]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaninker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield S.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.;"
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.E.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role in cell differentiation late in myogenesis.
CC Transcription factor Mef2 is essential for expression.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: In the embryo, expression is restricted to the
CC somatic, visceral, and pharyngeal muscles. Within the somatic
CC musculature, expression is localized at the ends of muscles fibers
CC at the point of attachment to the epidermis (at protein level).
CC There is no expression in cardiac mesoderm or in fat body.
CC -!- DEVELOPMENTAL STAGE: Expression is biphasic, peaking late in
CC embryogenesis (16-24 h embryos) and during the larval to pupal
CC transition, when the musculature is differentiating. Found in
CC developing muscles of the visceral and somatic mesoderm subsequent
CC to the formation of the muscle precursor cells. Decreased levels
CC are still detectable in adults.
CC -!- SIMILARITY: Contains 5 LIM zinc-binding domains.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; X91245; CAA62627.1; -;
DR EMBL; AF090832; AAC61591.1; -;
DR EMBL; AE003672; AAF54063.1; -;
DR EMBL; BT003202; AAO24957.1; -;
DR HSP; P32965; 1CTL.
DR IntAct; Q24400; -;
DR FlyBase; FBgn0014863; Mlp84B.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 5.
DR ProDom; PD000094; LIM; 5.
DR PROSITE; PS00478; LIM DOMAIN 1; 5.
DR PROSITE; PS50023; LIM DOMAIN 2; 5.
KW Developmental protein; Differentiation; LIM domain; Metal-binding;
KW Myogenesis; Nuclear protein; Repeat; Zinc.
FT DOMAIN 12 63
FT DOMAIN 65 80 Gly-rich.
FT DOMAIN 66 71 Nuclear localization signal (Potential).
FT DOMAIN 120 172 LIM 2.
FT DOMAIN 175 180 Nuclear localization signal (Potential).
FT DOMAIN 178 189 Gly-rich.
FT DOMAIN 222 274 LIM 3.
FT DOMAIN 276 291 Gly-rich.
FT DOMAIN 325 377 LIM 4.
FT DOMAIN 379 390 Gly-rich.

FT DOMAIN 421 473 LIM 5.
FT DOMAIN 475 490 Gly-rich.
SQ SEQUENCE 495 AA; 53525 MW; 2E559B9178E54C0E CRC64;

Query Match 29.8%; Score 60.5; DB 1; Length 495;
Best Local Similarity 32.5%; Pred. No. 21;
Matches 13; Conservative 4; Mismatches 16; Indels 7; Gaps 1;

Qy 2 SRGSSNSADLDKMDQAS-----CEARPHSDFCLGCAA 34
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 ARGSRWHKECFKGTCKKGLDLSILCEAPDKNIYKGCYA 174

Search completed: February 10, 2005, 18:17:15
Job time : 53.1974 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 17:53:53 ; Search time 55.5702 Seconds
(without alignments)
243.595 Million cell updates/sec

Title: us-10-062-831-59_COPY_36_70

Perfect score: 203

Sequence: 1 CSRGSSWSADLDKCDKASCARPHSDFLGCAAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980a:*
- 2: Geneseqp1990a:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001a:*
- 5: Geneseqp2002a:*
- 6: Geneseqp2003a:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203	100.0	114	2	AAW73409 Human sec
2	203	100.0	129	2	AAW88506 Human liv
3	203	100.0	129	3	AAV57940 Human tra
4	203	100.0	129	4	AAU03498 Human TWE
5	203	100.0	129	5	ABP61512 Human NP-
6	203	100.0	129	5	AAU79827 Human typ
7	203	100.0	129	6	ADA56889 Human sec
8	203	100.0	129	6	ABU56716 Lung carc
9	203	100.0	129	7	ADC74112 Human sec
10	203	100.0	129	7	ADC37867 Human sec
11	203	100.0	129	7	ADD89033 TAT274.1
12	203	100.0	129	7	ABU64232 Human FRA
13	203	100.0	129	7	ADN39126 Cancer/an
14	203	100.0	129	7	ADN39987 Cancer/an
15	203	100.0	129	8	ABM81706 Tumour-as
16	203	100.0	309	4	AAU03500 Human TWE
17	191	94.1	32	6	ADA49370 Human Fnl
18	190	93.6	129	5	AAU79828 Mouse typ
19	104.5	51.5	112	3	AAV91463 Human sec
20	104.5	51.5	112	6	ADA57390 Human sec
21	104.5	51.5	112	7	ADC74462 Human sec
22	104.5	51.5	112	7	ADD38025 Human sec
23	104.5	51.5	112	8	ADL71535 Novel hum
24	104.5	51.5	155	3	AAV91604 Human sec
25	104.5	51.5	155	6	ADA57391 Human sec

26	104.5	51.5	155	7	ADC74463 Human sec
27	104.5	51.5	155	7	ADD38026 Human sec
28	104.5	51.5	155	8	ADL71680 Novel hum
29	104.5	51.5	156	3	AAV91552 Human sec
30	104.5	51.5	156	8	ADL71624 Novel hum
31	68	33.5	248	7	ABO80503 Pseudomon
32	65	32.0	400	7	ABO77399 Pseudomon
33	64	31.5	974	7	AAE38808 Human POL
34	63.5	31.3	928	2	AAV97853 Rat REK7
35	63.5	31.3	1005	2	AAW83147 Rat recep
36	60.5	29.8	495	4	ABBS7748 Drosophil
37	60.5	29.8	495	4	ABBS7752 Drosophil
38	60	29.6	403	6	ABU52378 Human GPC
39	60	29.6	403	8	ADL24091 Human NOV
40	60	29.6	1188	8	ADO28625 Human EGF
41	59.5	29.3	405	2	AAW33737 Epidermal
42	59.5	29.3	405	5	AAE23001 Human Her
43	59.5	29.3	405	7	ADD25482 Binding d
44	59.5	29.3	405	7	ADD25488 Binding d
45	59.5	29.3	405	8	ADR24015 Human epi

ALIGNMENTS

RESULT 1
AAW73409
ID AAW73409 standard; protein; 114 AA.
XX
AC AAW73409;
XX
DT 19-FEB-1999 (first entry)
XX
DE Human secreted protein encoded by Gene No. 13.
XX
KW Secreted protein; human; protein therapy; gene therapy; blood disorder;
KW pathological condition; diagnosis; cancer; neurological disorder;
KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
KW immune system disorder; Alzheimer's disease; cognitive disorder;
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 114
FT note= "unspecified amino acid"
XX
WO9854206-A1.
XX
PN 03-DEC-1998.
XX
PD 28-MAY-1998; 98WO-US010868.
XX
PR 30-MAY-1997; 97US-0044039P.
PR 30-MAY-1997; 97US-0048093P.
PR 30-MAY-1997; 97US-0048101P.
PR 30-MAY-1997; 97US-0048190P.
PR 30-MAY-1997; 97US-0048356P.
PR 30-MAY-1997; 97US-0050935P.
PR 29-AUG-1997; 97US-0056250P.
PR 29-AUG-1997; 97US-0056293P.
PR 29-AUG-1997; 97US-0056296P.
XX
(HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;
PI Ni J, Feng F;
XX WPI; 1999-070209/06.
DR N-PSDB; AAV08823.
XX
PT New isolated human genes - useful for diagnosis and treatment of, e.g.
PT cancers, neurological disorders, immune diseases, developmental disorders

transmembrane proteins (see AAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines

Sequence 129 AA;

Query Match 100.0%; Score 203; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 35
|||||
DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 70
|||||

RESULT 3
AAW57940
ID AAW57940 standard; protein; 129 AA.
XX
AC AAW57940;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human transmembrane protein HTMPN-64.
XX
KW Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
KW antiproliferative; neuroprotective; immune disorder;
KW reproductive disorder; smooth muscle disorder; neurological disorder;
KW gastrointestinal disorder; developmental disorder;
KW cell proliferative disorder.
XX
OS Homo sapiens.
XX
FN WO9961471-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011904.
XX
PR 29-MAY-1998; 98US-0087260P.
PR 02-JUL-1998; 98US-0091674P.
PR 02-OCT-1998; 98US-0102954P.
PR 24-NOV-1998; 98US-0109869P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
XX
XX WPI; 2000-072605/06.
DR N-PSDB; AAW56761.
XX
PT Proteins, polynucleotides, vectors, host cells and antibodies used to
PT diagnose, treat or prevent immune, reproductive, smooth muscle,
PT neurological, gastrointestinal, developmental and cell proliferative
PT disorders.
XX
PS Claim 1; Page 163; 229pp; English.
XX
CC AAW56698 to AAW56776 encode AAW57877 to AAW57955 which represent human
CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
CC transmembrane protein have immunospecific, antiproliferative and
CC neuroprotective activities. The human transmembrane proteins,
CC polynucleotides encoding them and other compositions and methods from the
CC present invention, can be used for the diagnosis, treatment or prevention
CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,
CC developmental and cell proliferative disorders. The HTMPN's can be used
CC to treat or prevent disorders associated with a decreased expression or

or blood disorders.

Claim 11; Page 153; 189pp; English.

This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners

Sequence 114 AA;

Query Match 100.0%; Score 203; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 35
|||||
DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 70
|||||

RESULT 2
AAW88506
ID AAW88506 standard; protein; 129 AA.
XX
AC AAW88506;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human liver clone HP10432-encoded membrane protein.
XX
KW Transmembrane protein; HP10432; human; liver.
XX
OS Homo sapiens.
XX
FN WO9855508-A2.
XX
PD 10-DEC-1998.
XX
PF 03-JUN-1998; 98WO-JP002445.
XX
PR 03-JUN-1997; 97JP-00144948.
XX
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Sekine S, Yamaguchi T;
XX
XX WPI; 1999-045730/04.
DR N-PSDB; AAW84374.
XX
XX New human proteins containing transmembrane domains and their encoding
PT sequences - useful in the preparation of antibodies and large-scale
PT protein production, gene diagnosis, and gene therapy.
XX
PS Claim 1; Page 152-153; 178pp; English.
XX
CC This is the amino acid sequence of a transmembrane protein encoded by
CC human liver cDNA clone HP10432 (see AAW84374). The encoded protein has a
CC signal-like N-terminal region and one internal transmembrane domain. The
CC invention provides nucleotide sequences (see AAW84359-76) coding for 18

CC activity of HTPMN
 XX Sequence 129 AA;
 SQ Query Match 100.0%; Score 203; DB 3; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 35
 DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 70

RESULT 4
 ID AAU03498 standard; protein; 129 AA.
 XX AAU03498;
 DT 26-SEP-2001 (first entry)
 XX Human TWEAK receptor (TWEAKR) polypeptide.

DE TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
 KW rubecosis; uveitis; macular degeneration; arthritis; rheumatism;
 KW corneal graft neovascularisation; psoriasis; metastatic condition;
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
 KW peripheral atherosclerosis.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..78
 FT /note= "Extracellular domain"
 FT Peptide 1..27
 FT /note= "Signal peptide"
 FT Protein 28..129
 FT /note= "Mature human TWEAKR protein"
 FT Domain 79..101
 FT /note= "Transmembrane domain"
 FT Domain 102..129
 FT /note= "Intracellular domain"

XX WO200145730-A2.
 XX 28-JUN-2001.
 XX 19-DEC-2000; 2000WO-US034755.
 XX 20-DEC-1999; 99US-0172878P.
 XX 10-MAY-2000; 2000US-0203347P.
 XX (IMMV) IMMUNEX CORP.
 XX Wiley SR;
 XX WPI; 2001-417975/44.
 XX N-PSDB; AAS03963.
 XX Modulating angiogenesis in a mammal for treating diseases mediated by
 PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or
 PT peripheral tissue, by administering antagonist or agonist of TWEAK
 PT receptor.
 XX Example 1; Fig 1; 46pp; English.
 XX The sequence represents the human TWEAK receptor (TWEAKR) protein. The
 CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and

CC induces angiogenesis. TWEAKR may therefore be used to screen for and
 CC develop TWEAKR agonists and antagonists for the modulation of
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.
 CC The disorders mediated by angiogenesis include ocular disorders
 CC characterised by ocular neovascularisation such as diabetic retinopathy,
 CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity, and
 CC retrolental fibroplasia, rubecosis, uveitis, macular degeneration and
 CC corneal graft neovascularisation, and inflammatory diseases such as
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include
 CC malignant and metastatic conditions such as sarcomas and carcinomas,
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary
 CC atherosclerosis, peripheral atherosclerosis and ischaemia
 XX
 SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 35
 DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAAA 70

RESULT 5
 ABP61512
 ID ABP61512 standard; protein; 129 AA.
 XX ABP61512;
 XX 30-SEP-2002 (first entry)
 XX Human NF-kB activating protein SEQ ID NO 178.
 DE Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 XX Homo sapiens.
 OS WO200253737-A1.
 XX 11-JUL-2002.
 XX 25-DEC-2001; 2001WO-JP011389.
 XX 28-DEC-2000; 2000JP-00402288.
 XX 26-MAR-2001; 2001JP-00089912.
 XX 24-AUG-2001; 2001JP-00254018.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX WPI; 2002-583617/62.
 XX N-PSDB; ABQ92000.
 XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.
 XX Claim 4; Page 814-815; 841pp; Japanese.
 XX The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and

CC for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders

XX SQ Sequence 129 AA;
 Query Match 100.0%; Score 203; DB 5; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 35
 DB 36 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 70

RESULT 6
 AAU79827
 ID AAU79827 standard; protein; 129 AA.
 XX AC AAU79827;
 XX DT 15-JUL-2002 (first entry)
 XX DE Human type 1 transmembrane protein Fn14.
 XX KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;
 KW vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
 KW tumour necrosis factor family; TNF family; TWEAK receptor;
 KW myocardial ischaemic condition; myocardial infarction; wound healing;
 KW burn healing; gastric ulcer; tissue transplantation; vascular insufficiency;
 KW organ transplantation; neovascularisation; vascular insufficiency;
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.

OS Homo sapiens.
 XX WO20022166-A2.
 XX PD 21-MAR-2002.
 XX PF 12-SEP-2001; 2001WO-US028451.
 XX PR 14-SEP-2000; 2000US-0232355P.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Browning J, Burkly L, Jakubowski A, Zheng T;
 XX WPI; 2002-383103/41.
 XX PT Methods of modulating angiogenesis and inhibiting tumor progression,
 XX using TWEAK receptor agonists.
 XX PS Disclosure; Fig 10A; 37pp; English.
 XX CC The invention describes methods of modulating angiogenesis and inhibiting
 CC tumour progression using TWEAK (a novel member of the tumour necrosis
 CC factor or TNF family) receptor agonists. Conditions which can be treated
 CC using the agonists include myocardial ischaemic conditions (e.g.
 CC myocardial infarction), wound healing (e.g. burn healing and healing of
 CC gastric ulcers), and tissue and organ transplantations to promote
 CC neovascularisation, particularly in subjects suffering from vascular
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
 CC subsequently neovascularisation is useful in treatment of cancer,
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor
 CC described in the invention

XX SQ Sequence 129 AA;
 Query Match 100.0%; Score 203; DB 5; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 35
 DB 36 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 70

RESULT 7
 ADA56889
 ID ADA56889 standard; protein; 129 AA.
 XX AC ADA56889;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human secreted protein #172.

XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cytotatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.

XX OS Homo sapiens.
 XX WO2002102994-A2.
 XX PD 27-DEC-2002.
 XX PF 19-MAR-2002; 2002WO-US008278.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;
 XX WPI; 2003-167512/16.
 XX DR N-ESDB; ADA55993.

XX PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.

XX PS Claim 13; SEQ ID NO 1079; 1754pp; English.

XX CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 9% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for

CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 6; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCRCRPHSDFCIGCAA 35

Db 36 CSRGSSWSADLCKMDCASCRCRPHSDFCIGCAA 70

RESULT 8

ABU56716

ID ABU56716 standard; protein; 129 AA.

XX AC ABU56716;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #309.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX OS WO200286443-A2.

XX PN 31-OCT-2002.

XX PD 18-APR-2002; 2002WO-US012476.

XX PF 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 29-NOV-2001; 2001US-0334370P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR N-PSDB; ABX76445.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient

XX PT for treating lung cancer, by contacting a biological sample from the

XX PT patient with a polynucleotide that exhibits increased or decreased

XX PT expression in lung cancer.

XX PS Claim 27; Page 429; 453pp; English.

XX CC The invention relates to a method for detecting a lung cancer-associated

XX CC transcript in a cell from a patient, comprising contacting a biological

XX CC sample from the patient with a polynucleotide that selectively hybridises

XX CC to a sequence that is at least 80 % identical to a gene that exhibits

XX CC increased or decreased expression in lung cancer samples. Lung cancer-

XX CC associated polynucleotides and polypeptides are used for identifying a

XX CC compound that modulates a lung cancer-associated polypeptide, for

XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung

XX CC cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 6; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCRCRPHSDFCIGCAA 35

Db 36 CSRGSSWSADLCKMDCASCRCRPHSDFCIGCAA 70

RESULT 9

ADC74112

ID ADC74112 standard; protein; 129 AA.

XX AC ADC74112;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted protein - SEQ ID 745.

XX KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
XX KW antidiabetic; immunosuppressive; dermatologic; nephrotropic;
XX KW antiparkinsonian; neuroprotective; nontropic; antibacterial; virucide;
XX KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;
XX KW haemopoietic; haematologic; anaemia; autoimmune disorder;
XX KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
XX KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
XX KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
XX KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
XX KW human.

XX OS Homo sapiens.

XX PN WO2003038063-A2.

XX XX 08-MAY-2003.

XX PF 19-MAR-2002; 2002WO-US008277.

XX PR 21-MAR-2001; 2001US-0277340P.

XX PR 19-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX XX WPI; 2003-430516/40.

XX DR N-PSDB; ABC73497.

XX PT New human secreted polypeptide for diagnosing, preventing or treating

XX PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune

XX PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or

XX PT atherosclerosis).

XX PS Claim 16; SEQ ID NO 745; 2372pp; English.

XX XX The invention relates to a novel human secreted polypeptide comprising a

XX CC defined sequence given in the specification. The polypeptide, nucleic

XX CC acid molecule, antibody, agonist or antagonist of the invention may be

XX CC useful for preparing a composition for diagnosing or treating a

CC haemopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis, and
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 35
 Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 70

RESULT 10

ADD37867
 ID ADD37867 standard; protein; 129 AA.

XX AC ADD37867;

XX DT 15-JAN-2004 (first entry)

XX DE Human secreted protein #50.

XX KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 XX Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.

XX OS Homo sapiens.

XX FN WO200290526-A2.

XX PD 14-NOV-2002.

XX PF 19-MAR-2002; 2002WO-US008279.

XX PR 21-MAR-2001; 2001US-0277340P.

XX FR 19-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2003-140218/13.

XX PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 PT treating allergic or asthmatic disorders, or related immediate
 PT hypersensitivity disorders.

XX PS Claim 1; SEQ ID NO 349; 1323pp; English.

XX CC The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful
 CC for identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases the activity of the polypeptide. The polypeptides and nucleic
 CC acid molecules are also useful for detecting, preventing, diagnosing,
 CC prognosticating, treating or ameliorating inflammatory disorders
 CC neoplastic diseases, wound healing and disorders of epithelial cell

CC proliferation, immune disorders, cardiovascular disorders, blood-related
 CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
 CC disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers, or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein.

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 35
 Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 70

RESULT 11

ADD89033
 ID ADD89033 standard; protein; 129 AA.

XX AC ADD89033;

XX DT 29-JAN-2004 (first entry)

XX DE TAT274.

XX KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;
 XX cancer.

XX OS Homo sapiens.

XX FN WO2003057160-A2.

XX PD 17-JUL-2003.

XX PF 30-DEC-2002; 2002WO-US041798.

XX PR 02-JAN-2002; 2002US-0345444P.

XX PR 25-JAN-2002; 2002US-0351885P.

XX PR 25-FEB-2002; 2002US-0360066P.

XX PR 05-MAR-2002; 2002US-0362004P.

XX PR 20-MAR-2002; 2002US-0366869P.

XX PR 21-MAR-2002; 2002US-0366284P.

XX PR 28-MAR-2002; 2002US-0368679P.

XX PR 19-AUG-2002; 2002US-0404809P.

XX PR 21-AUG-2002; 2002US-0405645P.

XX PA (GETH) GENENTECH INC.

XX PI Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;
 XX Williams PM, Wu TD, Zhang Z;
 XX WPI; 2003-569537/53.
 XX DR N-PSDB; ADD89109.

XX PT New antibodies against tumor-associated antigenic target polypeptide,
 XX useful for treating or diagnosing tumors or cancers in mammals, e.g.
 XX prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 XX carcinomas.

XX PS Claim 1; SEQ ID NO 37; 252pp; English.

XX CC The present invention relates to antibodies against tumour-associated
 XX antigenic target polypeptide. The antibody is useful for treating or
 XX diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung
 XX cancer, breast cancer, colon cancer, ovarian cancer, prostate
 XX adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The
 XX present sequence represents a TAT polypeptide.

[illegible]

CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 35
 |||||
 Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 70

RESULT 14
 ADN39987
 ID ADN39987 standard; protein; 129 AA.

XX AC ADN39987;

DT 17-JUN-2004 (first entry)

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C357.

XX Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
 KW vulnery; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2002; 2002WO-US036810.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 21-NOV-2001; 2001US-0332464P.

XX PR 29-NOV-2001; 2001US-0334393P.

XX PR 03-DEC-2001; 2001US-0335394P.

XX PR 14-DEC-2001; 2001US-0340376P.

XX PR 08-JAN-2002; 2002US-0347211P.

XX PR 10-JAN-2002; 2002US-0347349P.

XX PR 08-FEB-2002; 2002US-0355250P.

XX PR 13-FEB-2002; 2002US-0356714P.

XX PR 20-FEB-2002; 2002US-0359077P.

XX PR 29-MAR-2002; 2002US-0368809P.

XX PR 04-APR-2002; 2002US-0370110P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PR 05-JUN-2002; 2002US-0386614P.

XX PR 16-JUL-2002; 2002US-0396839P.

XX PR 22-JUL-2002; 2002US-0397775P.

XX PR 22-JUL-2002; 2002US-0397845P.

XX PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D. Aziz N. Gineburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI; 2003-468649/44.

DR N-PSDB; ADN39770.

XX Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C357; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 35

|||||
 Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 70

RESULT 15

ABM81706

ID ABM81706 standard; protein; 129 AA.

XX AC ABM81706;

XX DT 18-NOV-2004 (first entry)

XX DE Tumour-associated antigenic target (TAT) polypeptide PRO12683, SEQ:4399.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX tumour; diagnosis; cell proliferative disorder; breast cancer;

XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;

XX central nervous system cancer; bladder cancer; pancreatic cancer;

XX cervical cancer; melanoma; leukaemia; hybridisation probe;

XX chromosome identification; chromosome mapping; gene mapping;

XX gene therapy; cytostatic.

XX OS Homo sapiens.

XX WO2004030615-A2.

XX PD 15-APR-2004.

XX PF 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN39936.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a

PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

XX
PS Claim 12; SEQ ID NO 4399; 7273pp; English.

XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX
SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 8; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSGADLDKCMDCASCRRPHSDFCLGCAA 35
|||||
Db 36 CSRGSSWSGADLDKCMDCASCRRPHSDFCLGCAA 70
|||||

Search completed: February 10, 2005, 18:11:33
Job time : 56.5702 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 18:17:36 ; Search time 40.6798 Seconds
(without alignments)
281.128 Million cell updates/sec

Title: US-10-062-831-59_COPY_36_70

Perfect score: 203

Sequence: 1 CSRGSSWSADLCKMDCASCRRPHSDFCLGCAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203	100.0	114	14	US-10-062-831-59
2	203	100.0	114	14	US-10-062-599-59
3	203	100.0	129	9	US-09-742-454A-4
4	203	100.0	129	9	US-09-883-777-4
5	203	100.0	129	14	US-10-044-298A-178
6	203	100.0	129	14	US-10-042-211A-178
7	203	100.0	129	15	US-10-331-496A-37
8	203	100.0	129	15	US-10-295-027-444
9	203	100.0	129	15	US-10-295-027-1305
10	203	100.0	129	15	US-10-617-217A-178
11	203	100.0	300	9	US-09-883-777-9
12	203	100.0	309	9	US-09-742-454A-7
13	203	100.0	309	9	US-09-883-777-7

Sequence 5, Appli
Sequence 5, Appli
Sequence 139, App
Sequence 284, App
Sequence 228, App
Sequence 2, Appli
Sequence 63, Appl
Sequence 136, App
Sequence 43, Appl
Sequence 49, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 18, Appl
Sequence 74, Appl
Sequence 116, App
Sequence 2, Appli
Sequence 17, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 76, Appl
Sequence 7, Appli
Sequence 125, App
Sequence 42048, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 538, App
Sequence 1557, Ap
Sequence 433, App
Sequence 433, App
Sequence 433, App

ALIGNMENTS

RESULT 1

US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match          100.0%; Score 203; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 70

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match          100.0%; Score 203; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 70

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-742-454A-4

Query Match          100.0%; Score 203; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 35
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Db 36 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 70

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-883-777-4

Query Match          100.0%; Score 203; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFLGCAAA 70

RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASahi Kasei Kabushiki Kaisha
; APPLICANT: Akio MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
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;; TITLE OF INVENTION: NF-K B Activating Gene
;; FILE REFERENCE: 1254-0191P
;; CURRENT APPLICATION NUMBER: US/10/024,298A
;; CURRENT FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: 60/314,385
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/278,641
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: 60/258,315
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: JP254018/2001
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: JP0088912/2001
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: JP402288/2000
;; PRIOR FILING DATE: 2000-12-28
;; NUMBER OF SEQ ID NOS: 182
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 178
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-024-298A-178

Query Match 100.0%; Score 203; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 6

US-10-042-211A-178
;; Sequence 178, Application US/10042211A
;; Publication No. US20030170719A1
;; GENERAL INFORMATION:
;; APPLICANT: MATSUDA, Akio et al.
;; TITLE OF INVENTION: NFkB Activating Gene
;; FILE REFERENCE: 1254-0192P
;; CURRENT APPLICATION NUMBER: US/10/042,211A
;; CURRENT FILING DATE: 2002-01-11
;; PRIOR APPLICATION NUMBER: JP 2000-402288
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: JP 2001-088912
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: JP 2001-254018
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/258,315
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 60/278,640
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: US 60/314,385
;; PRIOR FILING DATE: 2001-08-24
;; NUMBER OF SEQ ID NOS: 182
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 178
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match 100.0%; Score 203; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 7

US-10-331-496A-37
;; Sequence 37, Application US/10331496A
;; Publication No. US20030228305A1
;; GENERAL INFORMATION:
;; APPLICANT: FRANTZ, GRETCHEN
;; APPLICANT: HILAN, KENNETH J.
;; APPLICANT: PHILLIPS, HEIDI S.
;; APPLICANT: POLAKIS, PAUL
;; APPLICANT: SMITH, VICTORIA
;; APPLICANT: SPENCER, SUSAN D.
;; APPLICANT: WILLIAMS, P. MICKEY
;; APPLICANT: WU, THOMAS D.
;; APPLICANT: ZHANG, ZEMIN
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;; FILE REFERENCE: P5014E1-PCT
;; CURRENT APPLICATION NUMBER: US/10/331,496A
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 60/345,444
;; PRIOR FILING DATE: 2002-01-02
;; PRIOR APPLICATION NUMBER: US 60/351,885
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: US 60/360,066
;; PRIOR FILING DATE: 2002-02-25
;; PRIOR APPLICATION NUMBER: US 60/362,004
;; PRIOR FILING DATE: 2002-03-05
;; PRIOR APPLICATION NUMBER: US 60/366,869
;; PRIOR FILING DATE: 2002-03-20
;; PRIOR APPLICATION NUMBER: US 60/366,284
;; PRIOR FILING DATE: 2002-03-21
;; PRIOR APPLICATION NUMBER: US 60/368,679
;; PRIOR FILING DATE: 2002-03-28
;; PRIOR APPLICATION NUMBER: US 60/404,809
;; PRIOR FILING DATE: 2002-08-19
;; PRIOR APPLICATION NUMBER: US 60/405,645
;; PRIOR FILING DATE: 2002-08-21
;; NUMBER OF SEQ ID NOS: 95
;; SEQ ID NO 37
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-10-331-496A-37

Query Match 100.0%; Score 203; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 8

US-10-295-027-444
;; Sequence 444, Application US/10295027
;; Publication No. US20030232350A1
;; GENERAL INFORMATION:
;; APPLICANT: Afar, Daniel
;; APPLICANT: Aziz, Natasha
;; APPLICANT: Ginsberg, Wendy M.
;; APPLICANT: Gish, Kurt C.
;; APPLICANT: Glynn, Richard
;; APPLICANT: Hevezi, Peter A.
;; APPLICANT: Mack, David H.
;; APPLICANT: Murray, Richard
;; APPLICANT: Watson, Susan R.
;; APPLICANT: Eos Biotechnology, Inc.
;; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;; FILE REFERENCE: 018501-012500US
;; CURRENT APPLICATION NUMBER: US/10/295,027
;; CURRENT FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: US 09/663,733

RESULT 9
US-10-295-027-1305
Sequence 1305, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10

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RESULT 11
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2368-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20

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; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match 100.0%; Score 203; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 35
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 70

RESULT 12
US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match 100.0%; Score 203; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 35
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 70

RESULT 13
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match 100.0%; Score 203; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 35
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 70

RESULT 14
US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match 93.6%; Score 190; DB 9; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 35
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCIGCAAA 70

RESULT 15
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match      93.6%; Score 190; DB 9; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSRGSSWSADLDKCMDCASCARPHSDPCLGCAA 35
        |||||||
Db      36 CSSGSSWSADLDKCMDCASCARPHSDPCLGCAA 70
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Search completed: February 10, 2005, 18:43:37
Job time : 41.6798 secs


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RESULT 2
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
Db      36  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 3
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
Db      36  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
Db      36  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 5
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match      100.0%; Score 203; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
Db      36  CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 6
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
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; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match 100.0%; Score 203; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 7

US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match 100.0%; Score 203; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 8

US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match 93.6%; Score 190; DB 4; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.7e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 9

US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match 93.6%; Score 190; DB 4; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.7e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35
DB 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 10

US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319

; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match 51.5%; Score 104.5; DB 4; Length 112;
Best Local Similarity 90.5%; Pred. No. 1.1e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSCA-SC 20
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 11
US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-284

Query Match 51.5%; Score 104.5; DB 4; Length 155;
Best Local Similarity 90.5%; Pred. No. 1.5e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSCA-SC 20
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 12
US-09-489-847-228
; Sequence 228, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29

; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-228

Query Match 51.5%; Score 104.5; DB 4; Length 156;
Best Local Similarity 90.5%; Pred. No. 1.6e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSCA-SC 20
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 13
US-09-252-991A-29249
; Sequence 29249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29249
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29249

Query Match 33.5%; Score 68; DB 4; Length 248;
Best Local Similarity 39.5%; Pred. No. 0.71;
Matches 15; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

Qy 1 CSRGSS---WSADLDKCMDCSCARPHSD-FCIGCAA 34
Db 80 CWAGAAPTCWSATTCRCGCASSRRRTGRCWCAACSA 117

RESULT 14
US-09-252-991A-26145
; Sequence 26145, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

Job time : 15.4298 secs

; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 26145
 ; LENGTH: 400
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-26145

Query Match 32.0%; Score 65; DB 4; Length 400;
 Best Local Similarity 44.8%; Pred. No. 2.6;
 Matches 13; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 5 SSWADLDKCMDCASCARPHSDFLGCA 33
 Db 69 SNWTATLSPRTSTASCRPMFHCSCACCA 97

RESULT 15
 US-08-442-248-2
 ; Sequence 2, Application US/08442248
 ; Patent No. 5759863
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Winslow, John W.
 ; TITLE OF INVENTION: AL-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/442,248
 ; FILING DATE: 15-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/330128
 ; FILING DATE: 27-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Torchia, Timothy E.
 ; REGISTRATION NUMBER: 36,700
 ; REFERENCE/DOCKET NUMBER: 920C4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-8674
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 928 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-442-248-2

Query Match 31.3%; Score 63.5; DB 1; Length 928;
 Best Local Similarity 31.9%; Pred. No. 9.2;
 Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

QY 1 CSRGSSWADLDKCM-----DCASCR-----ARPHSDFLGCA 32
 Db 278 CSAEGEWLVPICKCKAGYEKNGTCQVCRPGFFKASPHSQTCSKC 324

Search completed: February 10, 2005, 18:18:46

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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:14:52 ; Search time 39 Seconds
(without alignments)
108.552 Million cell updates/sec

Title: US-10-062-831-59_COPY_71_114

Perfect score: 235

Sequence: 1 PPAPFRLWPILGGALSLTF.....LSGFLVWRCRRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	68	28.9	346	T00872	probable protein k
3	67.5	28.7	587	C70893	hypothetical prote
4	61	26.0	519	B87353	hypothetical prote
5	61	26.0	992	1 GNWVR3	structural polypro
6	61	26.0	1008	1 GNWVR3	glycoprotein precu
7	60	25.5	262	H71390	cytochrome-c oxida
8	60	25.5	516	E81789	multidrug resistan
9	60	25.5	529	C82487	conserved hypothet
10	60	25.5	730	2 JH0798	fasciclin IV precu
11	59.5	25.3	546	2 T47018	hypothetical prote
12	59.5	25.3	546	2 AG0236	probable membrane
13	59.5	25.3	685	2 S65974	conserved hypothet
14	59	25.1	261	2 T11199	cytochrome-c oxida
15	59	25.1	262	2 S43493	cytochrome-c oxida
16	59	25.1	298	2 AD7268	permease [imported
17	59	25.1	311	2 F97548	hypothetical prote
18	58.5	24.9	78	2 E69969	hypothetical prote
19	58.5	24.9	506	2 F83545	hypothetical prote
20	58.5	24.9	543	2 F81665	ADP, ATP carrier p
21	58.5	24.9	587	2 E96702	unknown protein, 6
22	58	24.7	36	2 C45875	M1 class I histoco
23	58	24.7	260	2 F82120	zinc ABC transport
24	58	24.7	388	2 A75318	conserved hypothet
25	58	24.7	445	2 D82184	quinol oxidase, ch
26	58	24.7	520	2 S45702	leukotriene-B4 20-
27	58	24.7	555	2 E70409	carbon starvation
28	58	24.7	597	2 G71373	probable methyl-ac
29	58	24.7	719	2 F96577	hypothetical prote

30	58	24.7	1379	1 S01254	hepatocyte growth
31	57.5	24.5	325	2 D89974	conserved hypothet
32	57.5	24.5	340	2 B70781	hypothetical prote
33	57.5	24.5	341	2 T45350	hypothetical prote
34	57.5	24.5	467	1 HLMSP3	poliovirus recepto
35	57.5	24.5	869	2 A82055	extracellular nucl
36	57.5	24.5	1445	1 A48148	protein-tyrosine-p
37	57	24.3	256	2 E75401	hypothetical prote
38	57	24.3	261	2 T11525	cytochrome-c oxida
39	57	24.3	261	2 G90612	cytochrome c oxida
40	57	24.3	262	2 A84967	hypothetical prote
41	57	24.3	384	2 E69834	hypothetical prote
42	57	24.3	590	2 B96573	protein F12M16.17
43	57	24.3	635	2 T20910	hypothetical prote
44	56.5	24.0	175	2 D75514	hypothetical prote
45	56	23.8	205	2 AE2442	hypothetical prote

ALIGNMENTS

RESULT 1

D75303

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: D75303

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: D75303

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-346 <WHI>

A:Cross-references: UNIPROT:Q9RSC0; GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF117;

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2205

A:Map position: 1

Query Match

Best Local Similarity 29.8%; Score 70; DB 2; Length 346;

Matches 16; Conservative 37.2%; Pred. No. 0.8;

Mismatches 7; Mismatches 20; Indels 0; Gaps 0;

QY 2 PAPFRLWPILGGALSLTFVLGLSGFLVWRCRRRSSPPPX 44

Db 148 PAPPLALAVSGGAALSVAGLGAHWSTRARPHLAAPPFH 190

RESULT 2

T00872

probable protein kinase At2g45590 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F17K2.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00872; D84892

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, March 1998

A:Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.

A:Reference number: Z14207

A:Accession: T00872

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-683 <RNU>

A:Cross-references: UNIPROT:O64639; EMBL:AC003680; NID:g2979540; PID:g2979551

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Molecule type: DNA
A;Residues: 1-519 <STO>
A;Cross-references: UNIPROT_Q9A9X4; GB:AE005673; NID:G13422090; PIDN:AAK23822.1; CSPDB:G

F;497-513/Domain: transmemb

A;Molecule type: DNA
A;Residues: 1-519 <STO>

A;Status: preliminary
A:Molecule type: DNA

A;Status: preliminary
A:Molecule type: DNA

F:514-1008/Product: glycoprotein G2 #status predicted <G2>
F:977-1008/Domain: transmembrane #status predicted <TM3>
F:34,70,108,208,493,691,696,912,949/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 26.0%; Score 61; DB 1; Length 1008;
Best Local Similarity 34.3%; Pred. No. 23;
Matches 12; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 6 RLLPILGALSITFVLGSLGFLVWRCRRRSS 40
DB 976 RAIWALGGTVSL--IIGVVIYVFTLCLKVKKS 1008

RESULT 7

H71390
Cytochrome-c oxidase (BC 1.9.3.1) chain III - common lancelet mitochondrion
C:Species: mitochondrion Branchiostoma lanceolatum (common lancelet)
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: H71390
R:Spruyt, N.; Delarbre, C.; Gachelin, G.; Laudet, V.
Nucleic Acids Res. 26, 3279-3285, 1998
A:Title: Complete sequence of the amphioxus (Branchiostoma lanceolatum) mitochondrial gene
A:Reference number: A71390; MUID:98292550; PMID:9628930
A:Accession: H71390
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-262 <SPR>
A:CROSS-references: UNIPROT:O47425; GB:Y16474; NID:G3292989; PIDN:CAA76253.1; PID:G32929
C:Genetics:
A:Gene: COI1
A:Genome: mitochondrion
A:Genetic code: SGC4
C:Superfamily: cytochrome-c oxidase chain III
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
F:17-35/Domain: transmembrane helix #status predicted <TR01>
F:42-67/Domain: transmembrane helix #status predicted <TR02>
F:74-106/Domain: transmembrane helix #status predicted <TR03>
F:130-153/Domain: transmembrane helix #status predicted <TR04>
F:157-184/Domain: transmembrane helix #status predicted <TR05>
F:192-224/Domain: transmembrane helix #status predicted <TR06>
F:234-257/Domain: transmembrane helix #status predicted <TR07>

Query Match 25.5%; Score 60; DB 2; Length 262;
Best Local Similarity 35.5%; Pred. No. 9.2;
Matches 11; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 2 PAPFRL-----WPIIGGALSITFVLGSLSGF 28
DB 6 PPHWHLVFPSPPLVGGSAAFLLTVGLVMWF 36

RESULT 8

E81789
multidrug resistance translocase NMA2168 [imported] - Neisseria meningitidis (strain Z24
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: E81789
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsi, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: E81789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <PAR>
A:CROSS-references: UNIPROT:Q9JSR9; GB:AL162758; GB:AL157959; NID:G7380672; PIDN:CAB8538
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: emrB; NMA2168
C:Superfamily: lincomycin-resistance protein lmrB

Query Match 25.5%; Score 60; DB 2; Length 516;

Best Local Similarity 25.7%; Pred. No. 17;
Matches 18; Conservative 11; Mismatches 15; Indels 26; Gaps 4;

QY 1 PPAPFRL---LW-----PILGGALS-----LTFVLGSLGFLVWR--RC 34
DB 139 PPAKRTLALALWMTVVVAVPLGVPILGWMISGNWGWIFFINIPIGIISAWITWKHLKC 198

QY 35 RRERSPPPX 44
DB 199 RETETVKMPT 208

RESULT 9

C82487
conserved hypothetical protein VCA0213 [imported] - Vibrio cholerae (strain N16961 serog
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82487
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <HEI>
A:CROSS-references: UNIPROT:Q9KMW5; GB:AE004361; GB:AE003853; NID:G9657600; PIDN:AAF9612
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0213
A:Map position: 2

Query Match 25.5%; Score 60; DB 2; Length 529;
Best Local Similarity 40.6%; Pred. No. 17;
Matches 13; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 11 ILGGALSITFVLGSLGFLVW--RCRRRSS 40
DB 86 LGGGLISLMTASGATRAFAVWAERKCKDRRSA 117

RESULT 10

JH0798
fasciclin IV precursor - American bird grasshopper
C:Species: Schistocerca americana (American bird grasshopper)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JH0798
R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good
Neuron 9, 831-845, 1992
A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in
A:Reference number: JH0798; MUID:93040225; PMID:1418998
A:Accession: JH0798
A:Molecule type: mRNA
A:Residues: 1-730 <KOL>
A:CROSS-references: UNIPROT:Q26473; GB:L00709; NID:G160844; PID:G160845
A:Experimental source: embryo
C:Comment: This protein plays a role in growth cone guidance in the developing central n
C:Keywords: glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-730/Product: fasciclin IV #status predicted <MAT>
F:23-627/Domain: extracellular #status predicted <EXT>
F:628-652/Domain: transmembrane #status predicted <TMM>
F:653-730/Domain: intracellular #status predicted <INT>
F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.5%; Score 60; DB 2; Length 730;
Best Local Similarity 48.4%; Pred. No. 23;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGFLVWRCRRRSSPPPX 44
DB 199 RETETVKMPT 208

639 GAL-----VVGFIGFLFSRRRCGSDYTDMPF 665

Db

RESULT 11

T47018

hypothetical protein [imported] - Yersinia pestis

C;Species: Yersinia pestis

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C;Accession: T47018

R;Buchrieser, C.; Ruesniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel submitted to the EMBL Data Library, October 1998

A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.

A;Reference number: 224348

A;Accession: T47018

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-546 <BUC>

A;Cross-references: UNIPROT:Q9ZC50; EMBL:AL031866; PIDN:CAA21361.1

A;Experimental source: strain 6/69

Query Match 25.3%; Score 59.5; DB 2; Length 546;

Best Local Similarity 34.9%; Pred. No. 20;

Matches 15; Conservative 6; Mismatches 7; Indels 15; Gaps 2;

Qy 2 PAPFLLWPILGGALSLTFVLGLLSG--FLVWRRCRRSSPPP 42

Db 246 PAPFMI-----VLGIVLQAFVWVTRRRQSGKTP 275

RESULT 12

AG0236

probable membrane protein YPO1940 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AG0236

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Taraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AG0236

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-546 <KUP>

A;Cross-references: UNIPROT:Q9ZC50; GB:AL590842; PIDN:CAC90755.1; PID:gl5979957; GSPDB:G

A;Gene: YPO1940

Query Match 25.3%; Score 59.5; DB 2; Length 546;

Best Local Similarity 34.9%; Pred. No. 20;

Matches 15; Conservative 6; Mismatches 7; Indels 15; Gaps 2;

Qy 2 PAPFLLWPILGGALSLTFVLGLLSG--FLVWRRCRRSSPPP 42

Db 246 PAPFMI-----VLGIVLQAFVWVTRRRQSGKTP 275

RESULT 13

S65974

conserved hypothetical protein yycA - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S65974; H70088

R;Ogasawara, N.; Nakai, S.; Yoshikawa, H. DNA Res. 1, 1-14, 1994

A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom

A;Reference number: S65967; MUID:96051385; PMID:7584024

A;Accession: S65974

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-685 <OGA>

A;Cross-references: UNIPROT:P37483; EMBL:D26185; NID:g467326; PIDN:BAA05180.1; PID:g4673

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Segikuchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togonoi, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, H.; Yoshikawa, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: H70088

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-685 <KUN>

A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16086.1; PID:g2636596

A;Experimental source: strain 168

C;Genetics:

A;Gene: yycA

Query Match 25.3%; Score 59.5; DB 2; Length 685;

Best Local Similarity 42.1%; Pred. No. 24;

Matches 16; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

Qy 2 PAPFLLWPILGGALS--LTF-VLGLLSGFLVWRRCRR 36

Db 353 FGPLELQFQSLGQISWMLPFLSLGLLGAISWVDRR 390

RESULT 14

T11199

cytochrome-c oxidase (EC 1.9.3.1) chain III - Vidua chalybeata mitochondrion

C;Species: mitochondrion Vidua chalybeata

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T11199

R;Mindell, D.P.; Sorenson, M.D.; Dimcheff, D.E. Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998

A;Title: Multiple independent origins of mitochondrial gene order in birds.

A;Reference number: Z17242

A;Accession: T11199

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-261 <MIN>

A;Cross-references: UNIPROT:Q9XL31; EMBL:AF090341; NID:g4894501; PID:g4894508; PIDN:AAD3

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC1

C;Superfamily: cytochrome-c oxidase chain III

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 25.1%; Score 59; DB 2; Length 261;

Best Local Similarity 32.1%; Pred. No. 12;

Matches 18; Conservative 5; Mismatches 9; Indels 24; Gaps 3;

Qy 2 PAPFLLWPILGGALSL-----TFVLGLLSGFLV---WRRCRRE 37

Db 13 PSP---WPILGAAALLTASGLTWMFHSNPRLLINGLISTILVMFQWWRDIVRE 64

RESULT 15

S43493

cytochrome-c oxidase (EC 1.9.3.1) chain III - sea squirt (Pyura stolonifera) mitochondrion

C;Species: mitochondrion Pyura stolonifera

C;Date: 10-Dec-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C;Accession: S43493; S48139

R;Durrheim, G.A.; Corfield, V.A.; Harley, E.H.; Ricketts, M.H. Nucleic Acids Res. 21, 3587-3588, 1993

Search completed: February 14, 2005, 07:24:03
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:14:02 ; Search time 175 Seconds
(without alignments)
128.751 Million cell updates/sec

Title: US-10-062-831-59_COPY_71_114

Perfect score: 235

Sequence: 1 PPAPFLWLPILGGALSLTF.....LSGFLVWRCRRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	84.7	129	1 FN14 HUMAN	Q9np84 homo sapien
2	199	84.7	191	2 Q6P2Q4	Q6p2q4 homo sapien
3	168	71.5	129	2 Q80XX9	Q80xx9 rattus norv
4	164	69.8	129	1 FN14 MOUSE	Q9cr75 m tumor nec
5	76.5	32.6	285	2 Q72JG0	Q72jg0 thermus the
6	71	30.2	473	2 Q98J10	Q98j10 rhizobium l
7	70	29.8	216	2 Q7NRH8	Q7nrh8 chromobacte
8	70	29.8	346	2 Q9RSC0	Q9rsc0 deinococcus
9	70	29.8	631	2 Q7S272	Q7s272 neurospora
10	68	28.9	583	2 Q64639	Q64639 arabidopsis
11	67.5	28.7	587	2 Q53417	Q53417 mycobacteri
12	67.5	28.7	587	2 Q7U0Q9	Q7u0q9 mycobacteri
13	67.5	28.7	603	2 Q8VK78	Q8vk78 mycobacteri
14	67	28.5	333	2 Q8BZG3	Q8bzg3 homo sapien
15	67	28.5	372	2 Q65LL2	Q65ll2 bacillus li
16	67	28.5	426	2 Q8BZG2	Q8bzg2 homo sapien
17	66	28.1	433	2 Q82Y76	Q82y76 nitrosomona
18	66	28.1	696	2 Q7XKLO	Q7xklo oryza sativ
19	65	27.7	77	2 Q92MC1	Q92mc1 rhizobium m
20	65	27.7	515	2 Q7U9M5	Q7u9m5 synochococc
21	65	27.7	726	2 Q7Q0C6	Q7q0c6 anopheles g
22	64.5	27.4	187	2 Q6L237	Q6l237 picophilus
23	64.5	27.4	260	2 Q8RRL2	Q8rrl2 pseudomonas
24	64.5	27.4	756	2 Q64R11	Q64r11 bacteroides
25	64.5	27.4	1451	2 Q7R2Y9	Q7r2y9 giardia lam
26	64	27.2	105	2 Q8B4Q0	Q8b4q0 pseudomonas
27	64	27.2	264	2 Q7F9H5	Q7f9h5 halocynthia
28	64	27.2	394	2 Q9EQX9	Q9eqx9 rattus norv
29	64	27.2	478	2 Q6K6G5	Q6k6g5 oryza sativ
30	63	26.8	210	2 Q63X19	Q63x19 burkholderi
31	63	26.8	243	2 Q8G9Y8	Q8g9y8 escherichia

RESULT 1

ID	FN14_HUMAN	STANDARD;	PRT;	129 AA.
AC	Q9NP84; Q9HC50;			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member Fn14 precursor			
DE	(Fibroblast growth factor-inducible immediate-early response protein			
DE	14) (FGF-inducible 14) (Tweak-receptor) (TweakR).			
GN	Name=TNFRSF12A; Synonyms=FN14;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=20216634; PubMed=10751351;			
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgerisson S.S., Bell D.W.,			
RA	Testa J.R., Beifley K.A., Winkles J.A.,			
RT	"The Fn14 immediate-early response gene is induced during liver			
RT	regeneration and highly expressed in both human and murine			
RT	hepatocellular carcinomas."			
RL	Am. J. Pathol. 156:1253-1261(2000).			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Tanaka S., Sugimachi K.;			
RT	"Human homologue of Fn14."			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Uterus;			
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

Q8hc7 triops can
Q71l1 calcarian m
Q71lr6 pipilo fusc
Q8zx90 pyrobaculum
Q9bzj7 homo sapien
Q8zaw0 homo sapien
Q8fe07 escherichia
Q6xn37 rhodococcus
Q8537 mus musculu
Q71eb6 grapevine r
Q88r15 pseudomonas
Q943g8 oryza sativ
Q96eq6 homo sapien

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RN FUNCTION.
RP MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;
RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RT Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RA "A novel TNF receptor family member binds TWEAK and is implicated in
RT angiogenesis.";
RL Immunity 15:837-846(2001).
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_006519;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC -!- INDUCTION: By FGF-1 and phorbol ester.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF191148; AAF69108.1; -
DR EMBL; AB035480; BAA94792.1; -
DR EMBL; AB035481; BAB17850.1; -
DR EMBL; BC002718; AAB02718.1; -
DR Genew; HGNC:18152; TNFRSF12A.
DR H-InvDB; HIX0012751; -
DR MIM; 605914; -
DR GO; GO:006928; P:cell motility; TAS.
DR GO; GO:0007275; P:development; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT 28 129 superfamily member Fn14.
FT DOMAIN 28 80 Extracellular (Potential).
FT TRANSMEM 81 101 Potential.
FT DOMAIN 102 129 Cytoplasmic (Potential).
FT REPEAT 36 67 TNFR-Cys (atypical).
FT DISULFID 36 49 Potential.
FT DISULFID 52 67 Potential.
FT VARSPIC 33 67 Missing (in isoform 2).
FT FTID=VSP_006519.
SQ SEQUENCE 129 AA; 13911 MW; BF3DFB9C1E1C448 CRC64;
Query Match 84.7%; Score 199; DB 1; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.5e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Oy 1 PPAPFRLWPILGGALSITFVLGLSGFLVWRCRRSSPPX 44
Db 71 PPAPFRLWPILGGALSITFVLGLSGFLVWRCRRREKFTPI 114
RESULT 2
Q6P2Q4

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ID Q6P2Q4 PRELIMINARY; PRT; 191 AA.
AC Q6P2Q4;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DB 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064377; AAG64377.1; -
KW Hypothetical protein.
FT NON TER 1
FT 1 NON TER 1
SQ SEQUENCE 191 AA; 20092 MW; 75B166C4E5F0FA01 CRC64;
Query Match 84.7%; Score 199; DB 2; Length 191;
Best Local Similarity 84.1%; Pred. No. 7.8e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Oy 1 PPAPFRLWPILGGALSITFVLGLSGFLVWRCRRSSPPX 44
Db 133 PPAPFRLWPILGGALSITFVLGLSGFLVWRCRRREKFTPI 176
RESULT 3
Q80XX9
ID Q80XX9 PRELIMINARY; PRT; 129 AA.
AC Q80XX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type 1 transmembrane protein FN14 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Mueiller A.M., Giegerich G.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J., Gaasterland S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertez G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verdardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
Nature 420:563-573(2002).

[3]

SEQUENCE FROM N.A.
TISUS-Breast tumor;
MEDLINE=22389825; PubMed=12477932; DOI=10.1073/pnas.2426038999;
Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavert T.B., Scheetz T.E.,
Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.J.,
Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Receptor for TNFSF12/TWEAK (By similarity). Weak inducer
of apoptosis in some cell types. Promotes angiogenesis and the
proliferation of endothelial cells. May modulate cellular adhesion
to matrix proteins.

-!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
TRAF3 (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine,
kidney, liver, lung and skin, and in adult heart and ovary.
Intermediate expression in adult kidney, lung and skin.

-!- INDUCTION: By FGF-1.

-!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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or send an email to license@isb-sib.ch.

EMBL; AF156164; AAF07882.1; -

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DR EMBL; AK005530; BAB24101.1; -.
DR EMBL; AK005382; BAB23989.1; -.
DR EMBL; BC025860; AAH25860.1; -.
DR MGD; MGI:1351484; Tnfirs12a.
DR GO; GO:0001726; F:protein binding; IDA.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0045773; P:positive regulation of axon extension; IDA.
DR GO; GO:006931; P:substrate-bound cell migration, cell attach. .; IDA.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00505; TNFR_NGFR_2; FALSE NEG.
KW Angiogenesis; Apoptosis; Cell adhesion; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT 28 129 superfamily member Fn14.
FT DOMAIN 28 80 Extracellular (Potential).
FT TRANSMEM 81 101 Potential.
FT DOMAIN 102 129 Cytoplasmic (Potential).
FT REPEAT 36 67 TNFR-Cys (atypical).
FT DISULFID 36 49 Potential.
FT DISULFID 52 67 Potential.
FT CONFLICT 3 4 SA -> PG (in Ref. 1).
SQ SEQUENCE 129 AA; 13641 MW; 1665C68B4D9A9253 CRC64;

Query Match 69.8%; Score 164; DB 1; Length 129;
Best Local Similarity 70.5%; Pred. No. 5.4e-11;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 PPAPRLWPILGGALSLTFVLGLLSGFLVWRCRRSSPPX 44
DB 71 PPAHFLWPILGGALSLVILVALVSSFLVWRCRRREKFTTPI 114

RESULT 5
Q72JG0 PRELIMINARY; PRT; 285 AA.
AC Q72JG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=TT00812;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wieser A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RA "The genome sequence of the extreme thermophile Thermus
RA thermophilus.";
RL Nat. Biotechnol. 22:547-553 (2004).
DR EMBL; AE017303; AAS81158.1; -.
DR InterPro; IPR010982; Lambda_like_DNA.
KW Complete proteome.
SQ SEQUENCE 285 AA; 31440 MW; C3C8A7292A7D6C24 CRC64;

Query Match 32.6%; Score 76.5; DB 2; Length 285;
Best Local Similarity 43.8%; Pred. No. 0.99;
Matches 21; Conservative 5; Mismatches 15; Indels 7; Gaps 3;

QY 1 PPAPRLWPILGGALSLTFVLGLL-SGFLVWRCRR---RSPSPX 44
DB 83 PPRPRRLWPML---LALLGLFLYAGFLWPRPEKVKVLPDP 127

RESULT 6
Q72JG0 PRELIMINARY; PRT; 473 AA.
AC Q72JG0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE M111933 protein.
GN OrderedLocustNames=m111933;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
DR EMBL; AP002998; BAB49185.1; -.
DR InterPro; IPR002810; DUF107.
DR Pfam; PF01957; MfeD; 1.
KW Complete proteome.
SQ SEQUENCE 473 AA; 48746 MW; 2C466F3B41A49AF5 CRC64;

Query Match 30.2%; Score 71; DB 2; Length 473;
Best Local Similarity 39.5%; Pred. No. 6.5;
Matches 15; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 5 FRLWLPILGGALSLTFVLGLLSGFLVWRCRRSSPP 42
DB 371 FAMSVAIVGPAALTLGLALLTGYVW---AARKNP 404

RESULT 7
Q7NRH8 PRELIMINARY; PRT; 216 AA.
AC Q7NRH8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=CV3803;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Canargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
RA Cretzynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Garzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leol L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,

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RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of *Chromobacterium violaceum* reveals
RT remarkable and exploitable bacterial adaptability";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL; AE016923; AAQ61465.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005293; F:lysine permease activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR001123; LYSE.
DR Pfam; PF01810; LyseE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 216 AA; 22482 MW; 73BF6D92977F7825 CRC64;
Query Match 29.8%; Score 70; DB 2; Length 216;
Best Local Similarity 47.5%; Pred. No. 4.3;
Matches 19; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
Qy 2 PAPFLLPILGGALSLTFLVGLSGFLVWRRCRRERSPP 41
Db 70 PALFAVKYIGGYLAWLGVNMLKSGILAWRRARRGDESP 109
RESULT 8
ID Q9RSC0 PRELIMINARY; PRT; 346 AA.
AC Q9RSC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical protein DR2205.
DE Hypothetical protein DR2205.
GN OrderedLocustNames=DR2205;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium *Deinococcus*
RT *radiodurans* R1";
RL Science 286:1571-1577(1999).
DR EMBL; AE002053; AAF11754.1; -;
DR PIR; D75303; D75303.
DR TIGR; DR2205; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 346 AA; 36056 MW; 1F6C08A36C46F01F CRC64;
Query Match 29.8%; Score 70; DB 2; Length 346;
Best Local Similarity 37.2%; Pred. No. 6.4;
Matches 16; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
Qy 2 PAPFLLPILGGALSLTFLVGLSGFLVWRRCRRERSPPPP 44
Db 148 PAPFLALAVSGGAALSVLALGALGAWHSTRAPHELAAPPPH 190
RESULT 9
Q7S272

ID Q7S272 PRELIMINARY; PRT; 631 AA.
AC Q7S272;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU09651.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kanal M., Kamyskas M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100430; EAA29481.1; -;
DR InterPro; IPR011043; Gal_oxid_central.
KW Hypothetical protein.
SQ SEQUENCE 631 AA; 68228 MW; B7CE72E9DF6A7677 CRC64;
Query Match 29.8%; Score 70; DB 2; Length 631;
Best Local Similarity 30.2%; Pred. No. 11;
Matches 16; Conservative 10; Mismatches 9; Indels 18; Gaps 2;
Qy 10 PILGGAL-SLTFLVGLSGFLVWRRCRRERS-----SPPPX 44
Db 521 PIVGGVGVVGLVGGVGLFWRRNKKNKNSAGALSALPVOBPSPPPPQ 573
RESULT 10
ID O64639 PRELIMINARY; PRT; 683 AA.
AC O64639;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein At2g45590.
GN Name=At2g45590;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
RA Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RT	"deciphering the biology of Mycobacterium tuberculosis from the									
RT	complete genome sequence."									
RL	Nature 393:537-544 (1998).									
DR	EMBL; BX842575; CAA17185.1; -.									
DR	PIR; C70893; C70893.									
DR	TubercuList; Rv1069c; -.									
KW	Complete proteome.									
QY	SEQUENCE 587 AA; DB13451EF3C3EEC6 CRC64;									
Query Match										
Best Local Similarity 28.7%; Score 67.5; DB 2; Length 587;										
Matches 24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;										
QY	2	PAPRLLWPI	-----LGGALSITFV-----	LGLLSG-----	FLV 30					
Db	35	PQIRSTTWIRHYFTGTANGLVFVWFSTP	LLPRGFLPQGLVSGICGAFGYGLGVFAV	94						
QY	31	W--RRCRSSPPPX	44							
Db	95	WLVRVYMRSHNSPPPP	110							
RESULT 12										
Q7U0Q9	PRELIMINARY; PRT; 587 AA.									
ID	Q7U0Q9									
DT	01-OCT-2003	(TrEMBLrel. 25, Created)								
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)								
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)								
DE	Hypothetical protein Wb1098c.									
GN	OrderedLocuNames=Wb1098c;									
OS	Mycobacterium bovis.									
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;									
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.									
OX	NCBI_TaxID=1765;									
RN	[1]									
RC	SEQUENCE FROM N.A.									
RP	STRAIN=AF2122/97;									
RX	MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;									
RA	Garnier T., Eighmeier K., Camus J.-C., Medina N., Mansoor H.,									
RA	Pyvor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,									
RA	Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,									
RA	Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;									
RA	"The complete genome sequence of Mycobacterium bovis.";									
RL	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).									
DR	EMBL; BX248337; CAD93958.1; -.									
KW	Complete proteome; Hypothetical protein.									
QY	SEQUENCE 587 AA; DB13451EF3C3EEC6 CRC64;									
Query Match										
Best Local Similarity 28.7%; Score 67.5; DB 2; Length 587;										
Matches 24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;										
QY	2	PAPRLLWPI	-----LGGALSITFV-----	LGLLSG-----	FLV 30					
Db	35	PQIRSTTWIRHYFTGTANGLVFVWFSTP	LLPRGFLPQGLVSGICGAFGYGLGVFAV	94						
QY	31	W--RRCRSSPPPX	44							
Db	95	WLVRVYMRSHNSPPPP	110							
RESULT 13										
Q8VK78	PRELIMINARY; PRT; 603 AA.									
ID	Q8VK78									
DT	01-MAR-2002	(TrEMBLrel. 20, Created)								
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)								
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)								
DE	Hypothetical protein.									
GN	OrderedLocuNames=WT1099;									
OS	Mycobacterium tuberculosis.									
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.									

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

```

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1551 / Oehkosh;
RX MEDLINE=2206494; PubMed=132218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishal W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
DR ENBL; AE000516; AAK45355.1; -.
DR TIGR; MT1099; -.
KW Hypothetical protein.
SQ SEQUENCE 603 AA; 66149 MW; F3C1A57609BEAB69 CRC64;

Query Match 28.7%; Score 67.5; DB 2; Length 603;
Best Local Similarity 31.6%; Pred.No.20;
Matches 24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;

QY 2 PAFRLLWPI-----LGGALSLTIV-----LGLLSG-----FLV 30
Db 35 PQIRSTWTHRYHTFTATGLVFWFSMTFSLLPGRFLPQGLVSGICGAPGYGLGVAV 94

QY 31 W--RRCRRRSSPPPX 44
Db 95 WLVRYMRSNHSNPPPP 110

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RESULT 14
Q9BZG3
ID Q9BZG3 PRELIMINARY; PRT; 333 AA.
AC Q9BZG3;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Acid phosphatase variant 3.
GN Name=ACPT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; Pubmed=11414767; DOI=10.1006/geno.2001.6556;
RT Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
RL is highly expressed in the testis.";
RL Genomics 74:385-395(2001)
DR ENBL; AF321918; AAR09396.1; -.
DR HSSP; P15309; IND6.
DR CG; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF003328; Acid phosphat A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

```

```

Query Match      28.5%; Score 67; DB 2; Length 333;
Best Local Similarity 40.5%; Pred.No. 14;
Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;

QY 1 PPAPFRLLPILGALSLLTFLVGLSLGFLVMR-RCRRERSSP 41
   | | | | | : | | | | |
Db 294 PPAP---VVPLLAGAVAVLVALSIGLIGLAWRPGCLRALGSP 332

```

RESULT 15

Q65LL2		PRELIMINARY;	PRT;	372 AA.
ID	Q65LL2			
AC	Q65LL2;			
DT	25-OCT-2004	(TrEMBLrel. 28, Created)		
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)		
DE	VhjN	(Proteinase inhibitor 14, serpin).		
GN	Name:yhjN; ORFNames=BL01326, BLI0114;			
OS	Bacillus licheniformis DSM 13.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCB1_TaxID=279010;			
[1]	RN			
SEQUENCE FROM N.A.				
RP	STRAIN=DSM 13;			
RC	PubMed=15383718;			
RA	Weith B., Herzberg C., Steckel S., Feesche S., Maurer K.H.,			
RA	Ehrenreich P., Baumeister S., Henne A., Liesegang H., Merkl R.,			
RA	Ehrenreich A., Gottschalk G.;			
RT	"The Complete Genome Sequence of Bacillus licheniformis DSM13, an			
RL	Organism with Great Industrial Potential.";			
RL	J. Mol. Microbiol. Biotechnol. 7:204-211(2004).			
[2]	RN			
SEQUENCE FROM N.A.				
RP	STRAIN=ATCC 14580;			
RC	Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,			
RA	Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,			
RA	Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,			
RA	Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,			
RA	Berka R.M.;			
RT	"Complete genome sequence of the industrial bacterium Bacillus			
RL	licheniformis and comparisons with closely related Bacillus species."			
RL	Genome Biol. 5:R77-R77(2004).			
DR	ENBL; AS017333; AAU40052.1; -.			
DR	ENBL; CP000002; AAU22705.1; -.			
SQ	SEQUENCE 372 AA; 39272 MW; AD3D10B8EBB6CFAB CRC64;			

```

Query Match      28.5%; Score 67; DB 2; Length 372;
Best Local Similarity 46.4%; Pred. No. 15;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy  5  FRLWPILGALSLTFFVLGSLSGFLVWR 32
      | | | | | | | | | | | | | |
Db  77  FKENWLIIVGMLLSVVFAMLSGFLVWR 104

Search completed: February 14, 2005, 07:23:19
Job time : 177 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:13:22 ; Search time 164 Seconds
(without alignments)
103.765 Million cell updates/sec

Title: US-10-062-831-59_COPY_71_114

Perfect score: 235

Sequence: 1 PPAPRLLPILGGALSTF.....LSGFLVWRRRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	100.0	114	2	AAW73409 Human sec
2	199	84.7	94	7	ABU64233 Human CRY
3	199	84.7	129	2	AAW88506 Human liv
4	199	84.7	129	3	AAV57940 Human tra
5	199	84.7	129	4	AAU03498 Human TWE
6	199	84.7	129	5	ABP61512 Human NF-
7	199	84.7	129	6	AAU79827 Human typ
8	199	84.7	129	5	ADA56889 Human sec
9	199	84.7	129	6	ABU56716 Lung can
10	199	84.7	129	7	ADC74112 Human sec
11	199	84.7	129	7	ADD37867 Human sec
12	199	84.7	129	7	ADD89033 TAT274.1
13	199	84.7	129	7	ABU64232 Human FRA
14	199	84.7	129	7	ADN39126 Cancer/an
15	199	84.7	129	7	ADN39987 Cancer/an
16	199	84.7	129	8	ABM81706 Tumour-as
17	164	69.8	129	5	AAU79828 Mouse typ
18	68	28.9	683	3	AG30077 Arabidops
19	68	28.9	683	5	ABE92130 Herbicida
20	67	28.5	333	5	ABG32546 Human tes
21	67	28.5	375	5	ABG32542 Human tes
22	67	28.5	426	4	ABG23348 Novel hum
23	67	28.5	426	5	AAU75788 Human pro
24	67	28.5	426	5	ABG32541 Human tes
25	67	28.5	426	5	AAU09880 Novel hum

26	67	28.5	426	8	ADS10721	Human the
27	64.5	27.4	351	8	ADH58984	Rat GPCR
28	64.5	27.4	351	8	ADI53331	Rat FPRL1
29	64.5	27.4	351	8	ADO57848	Rat formy
30	64.5	27.4	742	6	ABU20797	Protein e
31	63.5	27.0	935	8	ADO29071	Mouse nov
32	63	26.8	61	4	AAU53825	Propionib
33	63	26.8	61	6	ABM50344	Propionib
34	63	26.8	365	2	AAV43138	Human NAI
35	63	26.8	365	4	AAW23942	Human EST
36	63	26.8	365	5	AAU11929	Human pro
37	63	26.8	365	8	ADP56168	Human PRO
38	63	26.8	365	8	ADP25183	PRO polyP
39	63	26.8	368	3	AAW02827	Human G p
40	63	26.8	368	3	AAW19523	G protein
41	63	26.8	368	3	AAW71293	Human orp
42	63	26.8	368	4	AAW70142	Human G p
43	63	26.8	368	4	AAW64288	Human G p
44	63	26.8	368	4	AAU10303	G-protein
45	63	26.8	368	5	AAE19359	Human G-p

ALIGNMENTS

RESULT 1
AAW73409
ID AAW73409 standard; protein; 114 AA.
XX AC AAW73409;
XX AC AAW73409 (first entry)
DT 19-FEB-1999
DE Human secreted protein encoded by Gene No. 13.
KW Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 114
FT /note= "unspecified amino acid"
XX PN WO9854206-A1.
XX PD 03-DEC-1998.
XX PF 28-MAY-1998; 98WO-US010868.
XX PR 30-MAY-1997; 97US-0044039P.
XX PR 30-MAY-1997; 97US-0048093P.
XX PR 30-MAY-1997; 97US-0048101P.
XX PR 30-MAY-1997; 97US-0048190P.
XX PR 30-MAY-1997; 97US-0048356P.
XX PR 30-MAY-1997; 97US-0050935P.
XX PR 29-AUG-1997; 97US-0056250P.
XX PR 29-AUG-1997; 97US-0056293P.
XX PR 29-AUG-1997; 97US-0056296P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;
XX PI Ni J, Feng P;
XX DR WPI; 1999-070209/06.
XX DR N-PSDB; AAW08823.
XX PT New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders

PT or blood disorders.
 XX
 PS Claim 11; Page 153; 188pp; English.
 XX
 CC This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners
 XX
 SQ Sequence 114' AA;
 Query Match 100.0%; Score 235; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.1e-23;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44
 DB 71 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 114
 RESULT 2
 ABU64233
 ID ABU64233 standard; protein; 94 AA.
 XX
 AC ABU64233;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human CRYPTIC protein.
 XX
 KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;
 KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;
 KW antiinflammatory; cardiant; ophthalmological; neuroprotective;
 KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;
 KW antilipemic; weight loss; obesity; diabetes.
 XX
 OS Homo sapiens.
 OS
 FN WO2003077939-A1.
 XX
 PD 25-SEP-2003.
 XX
 PF 17-MAR-2003; 2003WO-EP050066.
 XX
 PR 19-MAR-2002; 2002US-0365851P.
 PR 14-MAY-2002; 2002US-0380565P.
 XX
 PA (GSEST) GENSET SA.
 XX
 PI Dialynas D, Lucas J, Scalia A;
 XX
 DR WPI; 2003-779086/73.
 DR N-PSDB; AAL56187.
 XX
 XX Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for treating or preventing a disorder associated with excessive weight loss or an obesity-related disorder.
 PT
 PT or an obesity-related disorder.
 XX
 XX Claim 2; Page 201; 206pp; English.
 PS
 XX

CC The present invention provides the human FRADJ and CRYPTIC proteins. These can be used in screening for antagonists or agonists of APM1 polypeptide or polypeptide fragment activity, comprising lipid partitioning, lipid metabolism or insulin-like activity. The agonist or antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for treating or preventing a disorder associated with excessive weight loss, comprising cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease-related weight loss, bulimia or anorexia, or an obesity-related disorder, comprising obesity, insulin resistance, atherosclerosis, atheromatous disease, heart disease, hypertension, stroke, syndrome x, insulin or non-insulin dependent diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related complications, e.g., microangiopathic lesions, ocular lesions, retinopathy, neuropathy or renal lesions. The present sequence is a polypeptide shown in the exemplification of the invention
 XX
 SQ Sequence 94 AA;
 Query Match 84.7%; Score 199; DB 7; Length 94;
 Best Local Similarity 84.1%; Pred. No. 3.1e-18;
 Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 PPAPFRLWPILGALSITFVLGSLGFLVWRCRRSSPPPX 44
 DB 36 PPAPFRLWPILGALSITFVLGSLGFLVWRCRRREKFTTPI 79
 RESULT 3
 AAW88506
 ID AAW88506 standard; protein; 129 AA.
 XX
 AC AAW88506;
 XX
 DT 30-MAR-1999 (first entry)
 XX
 DE Human liver clone HP10432-encoded membrane protein.
 XX
 KW Transmembrane protein; HP10432; human; liver.
 XX
 OS Homo sapiens.
 OS
 FN WO9855508-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 03-JUN-1998; 98WO-JP002445.
 XX
 PR 03-JUN-1997; 97JP-0014948.
 XX
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S, Sekine S, Yamaguchi T;
 XX
 DR WPI; 1999-045730/04.
 DR N-PSDB; AAV84374.
 XX
 PT New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.
 PT
 PS Claim 1; Page 152-153; 178pp; English.
 XX
 CC This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAV84359-76) coding for 18 transmembrane proteins (see AAW8491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are

CC used for the detection of ligands corresponding to the expressed
CC proteins, and the screening of low mol.wt. medicines

SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 2; Length 129;
Best Local Similarity 84.1%; Pred. NO. 4.3e-18;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRERSPPPX 44
DB 71 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 4

AAV57940
ID AAV57940 standard; protein; 129 AA.

XX AC AAV57940;

DT 23-MAR-2000 (first entry)

DE Human transmembrane protein HTPMN-64.

XX Human; transmembrane protein; HTPMN; diagnosis; immunospecific;
KW antiproliferative; neuroprotective; immune disorder;
KW reproductive disorder; smooth muscle disorder; neurological disorder;
KW gastrointestinal disorder; developmental disorder;
KW cell proliferative disorder.

XX OS Homo sapiens.

XX PN WO9561471-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011904.

XX PR 29-MAY-1998; 98US-0087260P.

XX PR 02-JUL-1998; 98US-0091674P.

XX PR 02-OCT-1998; 98US-0102954P.

XX PR 24-NOV-1998; 98US-0109869P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

XX PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;

XX DR WPI; 2000-072605/06.

XX DR N-PSDB; AAZ56761.

XX PT Proteins, polynucleotides, vectors, host cells and antibodies used to

XX PT diagnose, treat or prevent immune, reproductive, smooth muscle,

XX PT neurological, gastrointestinal, developmental and cell proliferative

XX PT disorders.

XX PS Claim 1; Page 163; 229pp; English.

XX CC AAZ56698 to AAZ56776 encode AAV57877 to AAV57955 which represent human

XX CC transmembrane proteins designated HTPMN-1 to HTPMN-79, respectively. The

XX CC transmembrane protein have immunospecific, antiproliferative and

XX CC neuroprotective activities. The human transmembrane proteins,

XX CC polynucleotides encoding them and other compositions and methods from the

XX CC present invention, can be used for the diagnosis, treatment or prevention

XX CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,

XX CC developmental and cell proliferative disorders. The HTPMN's can be used

XX CC to treat or prevent disorders associated with a decreased expression or

XX CC activity of HTPMN

XX SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 3; Length 129;
Best Local Similarity 84.1%; Pred. NO. 4.3e-18;

Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRERSPPPX 44
DB 71 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 5

AAU03498
ID AAU03498 standard; protein; 129 AA.

XX AC AAU03498;

DT 26-SEP-2001 (first entry)

DE Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;
KW corneal graft neovascularisation; psoriasis; metastatic condition;
KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
KW preneoplastic condition; myocardial angiogenesis; wound granulation;
KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
KW peripheral atherosclerosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX FH Domain 1..78

XX FT Peptide 1..27 /note= "Extracellular domain"

XX FT Protein 28..129 /note= "Signal peptide"

XX FT Domain 79..101 /note= "Mature human TWEAKR protein"

XX FT Domain 102..129 /note= "Transmembrane domain"

XX FT Domain 102..129 /note= "Intracellular domain"

XX PN WO200145730-A2.

XX PD 28-JUN-2001.

XX PF 19-DEC-2000; 2000WO-US034755.

XX PR 20-DEC-1999; 99US-0172878P.

XX PR 10-MAY-2000; 2000US-0203347P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Wiley SR;

XX DR WPI; 2001-417975/44.

XX DR N-PSDB; AAS03963.

XX PT Modulating angiogenesis in a mammal for treating diseases mediated by

XX PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or

XX PT peripheral tissue, by administering antagonist or agonist of TWEAK

XX PT receptor.

XX PS Example 1; Fig 1; 46pp; English.

XX CC The sequence represents the human TWEAK receptor (TWEAKR) protein. The

XX CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and

XX CC induces angiogenesis. TWEAKR may therefore be used to screen for and

XX CC develop TWEAKR agonists and antagonists for the modulation of

XX CC angiogenesis, to be used in the treatment and diagnosis of human disease.

XX CC The disorders mediated by angiogenesis include ocular disorders

XX CC characterised by ocular neovascularisation such as diabetic retinopathy,

XX CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,

XX Sequence 129 AA;

Qy 1 PPAPRLWPILGGALSITFVLGLLSGFLVWRRCRRERSPPPX 44
 |||||
 Db 71 PPAPRLWPILGGALSITFVLGLLSGFLVWRRCRRREKFTTPI 114
 |||||

RESULT 8

ADA56889
ID ADA56889 standard; protein; 129 AA.
XX AC ADA56889;
XX DT 20-NOV-2003 (first entry)
XX DE Human secreted protein #172.
XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
XX KW cytostatic; cerebroprotective; neuroprotective; nootropic;
XX KW cardiovascular; antiarteriosclerotic; gene therapy;
XX KW human secreted protein; immune disorder; inflammation;
XX KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
XX KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
XX KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
XX KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
XX KW triple helix formation; antisense gene therapy; forensic biology.
XX OS Homo sapiens.
XX PN WO2002102994-A2.
XX PD 27-DEC-2002.
XX PF 19-MAR-2002; 2002WO-US008278.
XX PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM;
XX WPI; 2003-167512/16.
XX DR N-PSDB; ADA55993.
XX PT New human secreted polypeptides and polynucleotides, useful for
XX PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX PT conditions, respiratory disorders, cancers, CNS disorders, or
XX PT neurodegenerative disorders.
XX PS Claim 13; SEQ ID NO 1079; 1754pp; English.
XX CC The invention relates to 592 new human secreted polypeptides useful for
XX CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX CC conditions, respiratory disorders, cancers, CNS disorders, or
XX CC neurodegenerative disorders, or polypeptides comprising an amino acid
XX CC sequence at least 95% identical to the new sequences. The polypeptides,
XX CC antibodies or antibody fragments that bind to the polypeptides, nucleic
XX CC acids encoding the polypeptides, agonists or antagonists that binds to
XX CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX CC compositions for diagnosing, treating or preventing an e.g. immune
XX CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
XX CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX CC polynucleotides are useful for chromosome identification, chromosome
XX CC mapping, for controlling gene expression through triple helix formation
XX CC or antisense DNA or RNA, in gene therapy, for identifying individuals
XX CC from minute biological samples, in forensic biology, and as hybridization
XX CC probes. The polypeptides are useful for as molecular weight markers on
XX CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
XX CC gels, to raise antibodies, for testing biological activities, and for
XX CC treating or preventing neural disorders, immune system disorders,
XX CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX CC renal, proliferative and/or cancerous diseases. This sequence corresponds
XX CC to one of the polypeptide of the invention. Note: The sequence data for
XX CC this patent did form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 129 AA;
XX Query Match 84.7%; Score 199; DB 6; Length 129;
XX Best Local Similarity 84.1%; Pred. NO. 4.3e-18;
XX Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PPAPFRLWPILGGLSLTFLVLLSGFLVWRRRRSSPPX 44
DB 71 PPAPFRLWPILGGLSLTFLVLLSGFLVWRRRRREKFTTPI 114
RESULT 9
ABU56716
ID ABU56716 standard; protein; 129 AA.
XX AC ABU56716;
XX DT 02-APR-2003 (first entry)
XX DE Lung cancer-associated polypeptide #309.
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX OS Unidentified.
XX PN WO200286443-A2.
XX PD 31-OCT-2002.
XX PF 18-APR-2002; 2002WO-US012476.
XX PR 18-APR-2001; 2001US-0284770P.
XX PR 10-MAY-2001; 2001US-0290492P.
XX PR 09-NOV-2001; 2001US-0339245P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 29-NOV-2001; 2001US-0334370P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX DR N-PSDB; ABX76445.
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer.
XX PS Claim 27; Page 429; 453pp; English.
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80% identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX CC bronchiectasis. The genes, polynucleotides and polypeptides are useful

CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein.

XX
SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;
Best Local Similarity 84.1%; Pred. No. 4.3e-18;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERSPPPX 44
|||
DB 71 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERKFTTPI 114
|||

RESULT 12

ADD89033
ID ADD89033 standard; protein; 129 AA.

XX AC

XX ADD89033;

XX DT 29-JAN-2004 (first entry)

XX DE TAT274.

XX tumour-associated antigenic target polypeptide; Cytostatic; tumour;

XX cancer.

XX OS Homo sapiens.

XX PN WO2003057160-A2.

XX PD 17-JUL-2003.

XX PF 30-DEC-2002; 2002WO-US041798.

XX PR 02-JAN-2002; 2002US-0345444P.

XX PR 25-JAN-2002; 2002US-0351885P.

XX PR 25-FEB-2002; 2002US-0360066P.

XX PR 05-MAR-2002; 2002US-0362004P.

XX PR 20-MAR-2002; 2002US-0366869P.

XX PR 21-MAR-2002; 2002US-0366284P.

XX PR 28-MAR-2002; 2002US-0368679P.

XX PR 19-AUG-2002; 2002US-0404809P.

XX PR 21-AUG-2002; 2002US-0405645P.

XX PA (GETH) GENENTECH INC.

XX PI Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;

XX PI Williams PM, Wu TD, Zhang Z;

XX WPI: 2003-569537/53.

XX DR N-PSDB; ADD89109.

XX New antibodies against tumor-associated antigenic target polypeptide,

XX useful for treating or diagnosing tumors or cancers in mammals, e.g.

XX prostate cancer, lung cancer, prostate adenocarcinomas or renal cell

XX carcinomas.

XX Claim 1; SEQ ID NO 37; 252pp; English.

XX The present invention relates to antibodies against tumour-associated

XX antigenic target polypeptide. The antibody is useful for treating or

XX diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung

XX cancer, breast cancer, colon cancer, ovarian cancer, prostate

XX adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The

XX present sequence represents a TAT polypeptide.

XX SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;

Best Local Similarity 84.1%; Pred. No. 4.3e-18;

Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERSPPPX 44
|||
DB 71 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERKFTTPI 114
|||

RESULT 13

ABU64232

XX ID ABU64232 standard; protein; 129 AA.

XX AC ABU64232;

XX DT 11-MAR-2004 (first entry)

XX DE Human FRADJ protein.

XX KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;

XX KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;

XX KW antiinflammatory; cardiatic; ophthalmologic; neuroprotective;

XX KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;

XX KW antilipemic; weight loss; obesity; diabetes.

XX OS Homo sapiens.

XX PN WO2003077939-A1.

XX PD 25-SEP-2003.

XX PF 17-MAR-2003; 2003WO-EP050066.

XX PR 19-MAR-2002; 2002US-0365851P.

XX PR 14-MAY-2002; 2002US-0380565P.

XX PA (GEST) GENSET SA.

XX PI Dialynas D, Lucas J, Scalia A;

XX WPI; 2003-779086/73.

XX DR N-PSDB; AAL56186.

XX PT Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for loss

XX treating or preventing a disorder associated with excessive weight loss

XX or an obesity-related disorder.

XX PS Claim 1; Page 200; 206pp; English.

XX The present invention provides the human FRADJ and CRYPTIC proteins.

XX These can be used in screening for antagonists or agonists of APM1

XX polypeptide or polypeptide fragment activity, comprising lipid

XX partitioning, lipid metabolism or insulin-like activity. The agonist or

XX antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for

XX treating or preventing a disorder associated with excessive weight loss,

XX comprising cachexia, cancer-related weight loss, AIDS-related weight

XX loss, chronic inflammatory disease-related weight loss, bulimia or

XX anorexia, or an obesity-related disorder, comprising obesity, insulin

XX resistance, atherosclerosis, atheromatous disease, heart disease,

XX hypertension, stroke, syndrome x, insulin or non-insulin dependent

XX diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related

XX complications, e.g., microangiopathic lesions, ocular lesions, is a

XX retinopathy, neuropathy or renal lesions. The present sequence is a

XX polypeptide shown in the exemplification of the invention

XX SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;

Best Local Similarity 84.1%; Pred. No. 4.3e-18;

Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERSPPPX 44
|||
DB 71 PPAPFRLWPILGGALSLTFVLGSLSGFLVWRCRRERKFTTPI 114
|||

RESULT 14
ADN39126
ID ADN39126 standard; protein; 129 AA.
XX
XX
AC ADN39126;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:444.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-035250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-036809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-037246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
XX N-PSDB; ADN39125.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO 444; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides, and
XX antibodies and methods are useful for diagnosing, prognosing and treating
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 129 AA;
Query Match 84.7%; Score 199; DB 7; Length 129;
Best Local Similarity 84.1%; Pred. No. 4.3e-18;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PPAPRLWPTLGLGALSITFVLGSLGFLVWRCRRSSPPX 44
DB 71 PPAPRLWPTLGLGALSITFVLGSLGFLVWRCRRREKFTTPI 114
RESULT 15
ADN39987
ID ADN39987 standard; protein; 129 AA.
XX
XX ADN39987;
AC
XX
DT 17-JUN-2004 (first entry)
XX
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C357.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-035250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-036809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-037246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
XX N-PSDB; ADN39770.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO C357; 1385pp; English.

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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:23:28 ; Search time 130 Seconds
(without alignments)
110.592 Million cell updates/sec

Title: US-10-062-831-59_COPY_71_114

Perfect score: 235

Sequence: 1 PPAPRLLPILGGALSLTF.....LSGFLVWRCRRRSSPPPX 44

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Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	235	100.0	114	14	US-10-062-599-59
3	199	84.7	129	9	US-09-742-454A-4
4	199	84.7	129	9	US-09-883-777-4
5	199	84.7	129	14	US-10-024-238A-178
6	199	84.7	129	14	US-10-042-211A-178
7	199	84.7	129	15	US-10-331-496A-37
8	199	84.7	129	15	US-10-295-027-444
9	199	84.7	129	15	US-10-295-027-1305
10	199	84.7	129	15	US-10-617-217A-178
11	164	69.8	129	9	US-09-742-454A-5
12	164	69.8	129	9	US-09-883-777-5
13	67	28.5	426	15	US-10-257-174-44

Sequence 6, Appli
Sequence 48721, A
Sequence 5, Appli
Sequence 59, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 627, App
Sequence 6, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 60, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 2579, Ap
Sequence 2, Appli
Sequence 154909,
Sequence 454, App
Sequence 56, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 17, Appl
Sequence 19, Appl
Sequence 8, Appli
Sequence 175064,
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 177016,
Sequence 47140, A

ALIGNMENTS

RESULT 1
US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 59
; LENGTH: 114

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match      100.0%; Score 235; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44
    |||||
Db 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 114

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/590,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match      100.0%; Score 235; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44
    |||||
Db 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 114

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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```
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-742-454A-4

Query Match      84.7%; Score 199; DB 9; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44
    |||||
Db 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-883-777-4

Query Match      84.7%; Score 199; DB 9; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44
    |||||
Db 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
```


US-10-024-211A-178
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP008912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-178

Query Match 84.7%; Score 199; DB 14; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPX 44
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 6

US-10-042-211A-178
; Sequence 178, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:

; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match 84.7%; Score 199; DB 14; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPX 44
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 7

US-10-331-496A-37
; Sequence 37, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 37
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-37

Query Match 84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPX 44
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 8

US-10-295-027-444
; Sequence 444, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733

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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRSSPPX 44
Db 71 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 9
US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/563,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
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; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRSSPPX 44
Db 71 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 10
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-178

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRSSPPX 44
Db 71 PPAPFLLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 11
US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
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; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match 69.8%; Score 164; DB 9; Length 129;
Best Local Similarity 70.5%; Pred. No. 1.7e-11;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 PPAPRLWPILGGALSITFVLGLSGFLVWRCRRSSPPX 44
Db 71 PPAHRLWPILGGALSITFVLGLSGFLVWRCRRREKFTPI 114

RESULT 12

US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match 69.8%; Score 164; DB 9; Length 129;
Best Local Similarity 70.5%; Pred. No. 1.7e-11;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 PPAPRLWPILGGALSITFVLGLSGFLVWRCRRSSPPX 44
Db 71 PPAHRLWPILGGALSITFVLGLSGFLVWRCRRREKFTPI 114

RESULT 13

US-10-257-174-44
; Sequence 44, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
; APPLICANT: AGARWAL, PANKAJ
; APPLICANT: MURDOCH, PAUL R.
; APPLICANT: RIZVI, SAFIA K.
; APPLICANT: SMITH, RANDALL F.
; APPLICANT: XIANG, ZHAOYING
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/10/257,174
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417

; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-174-44

Query Match 28.5%; Score 67; DB 15; Length 426;
Best Local Similarity 40.5%; Pred. No. 11;
Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;
Qy 1 PPAPRLWPILGGALSITFVLGLSGFLVWRCRRSSSP 41
Db 387 PPAP---VVPILAGAVLVLSGLGLLAWRPGCLRALGGP 425

RESULT 14

US-10-343-357-6
; Sequence 6, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. TOM
; APPLICANT: ELLIOTT, VICKI S.; RAMKUMAR, JAYALAXMI
; APPLICANT: YAO, MONIQUE G.; BURFORD, NEIL
; APPLICANT: WANG, YUMEI E.; STEWART, ELIZABETH A.
; APPLICANT: GANDHI, AMEENA R.; ARVIZU, CHANDRA S.
; APPLICANT: LEE, ERNESTINE A.; HAFALIA, APRIL J.A.
; APPLICANT: LU, DYUNG AINA M.; TRIBOULEY, CATHERINE M.
; APPLICANT: GRIFFIN, JENNIFER A.; BAUGHN, MARIAH R.
; APPLICANT: YUE, HENRY; WARREN, BRIDGET A.
; APPLICANT: NGUYEN, DANIEL B.; CHAWLA, NARINDER K.
; APPLICANT: KEARNEY, LIAM
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480440CD1
US-10-343-357-6

Query Match 28.5%; Score 67; DB 15; Length 426;
Best Local Similarity 40.5%; Pred. No. 11;
Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;
Qy 1 PPAPRLWPILGGALSITFVLGLSGFLVWRCRRSSSP 41
Db 387 PPAP---VVPILAGAVLVLSGLGLLAWRPGCLRALGGP 425

RESULT 15

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US-10-282-122A-48721
; Sequence 48721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48721
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48721

Query Match      27.4%; Score 64.5; DB 15; Length 742;
Best Local Similarity 40.9%; Pred. No. 38;
Matches 18; Conservative 7; Mismatches 8; Indels 11; Gaps 3;

Qy 4 PFRLWPI-----IGGALSLTFVLGLLSG--FLVWRECRERS 39
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Db 337 PEKTRHPVWVFWFALIG---SITAIIVSLLSGITYLYWRETKKRS 377

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Search completed: February 14, 2005, 07:35:50
Job time : 131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:15:17 ; Search time 43 Seconds
(without alignments)
76.385 Million cell updates/sec

Title: US-10-062-831-59_COPY_71_114

Perfect score: 235
Sequence: 1 PPAPFRLWPIILGALSITF.....LSGFLVWRCRRRSSPPPX 44

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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6: /cgm2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	235	100.0	114	4	US-09-690-454-59
2	199	84.7	129	4	US-09-883-777-4
3	199	84.7	129	4	US-09-949-016-6914
4	199	84.7	129	4	US-09-742-454A-4
5	164	69.8	129	4	US-09-883-777-5
6	164	69.8	129	4	US-09-742-454A-5
7	63	26.8	365	4	US-09-949-016-6907
8	63	26.8	391	4	US-09-949-016-7325
9	61	26.0	992	1	US-08-127-499A-1
10	61	26.0	992	1	US-08-482-847-1
11	60	25.5	309	4	US-09-883-777-7
12	60	25.5	309	4	US-09-742-454A-7
13	60	25.5	730	1	US-08-121-713D-58
14	60	25.5	730	1	US-08-835-268-58
15	60	25.5	730	2	US-09-060-692-58
16	60	25.5	730	3	US-08-833-391-58
17	60	25.5	730	3	US-09-060-610-58
18	60	25.5	730	5	PCT-US94-10151A-58
19	60	25.5	839	4	US-09-489-039A-13252
20	59.5	25.3	137	4	US-09-489-039A-11239
21	58.5	24.9	153	4	US-09-252-991A-18571
22	58.5	24.9	231	4	US-09-724-623-116
23	58.5	24.9	617	4	US-09-252-991A-29507
24	58	24.7	153	4	US-09-452-937A-30
25	57.5	24.5	256	4	US-09-071-035-300
26	57.5	24.5	284	4	US-09-071-035-298
27	57.5	24.5	284	4	US-09-933-999A-6

28	57.5	24.5	315	4	US-09-134-000C-6125	Sequence 6125, Ap
29	57.5	24.5	1006	4	US-09-949-016-7897	Sequence 7897, Ap
30	57.5	24.5	1445	1	US-08-015-986A-2	Sequence 2, Appli
31	57.5	24.5	1445	2	US-08-446-363-2	Sequence 2, Appli
32	57	24.3	153	4	US-08-252-991A-31363	Sequence 31363, A
33	57	24.3	652	2	US-08-751-305-2	Sequence 2, Appli
34	56	23.8	197	4	US-09-252-991A-30359	Sequence 30359, A
35	56	23.8	278	3	US-08-663-082-4	Sequence 4, Appli
36	56	23.8	402	4	US-09-252-991A-18195	Sequence 18195, A
37	56	23.8	403	4	US-09-252-991A-30953	Sequence 30953, A
38	56	23.8	483	4	US-09-543-681A-5752	Sequence 5752, Ap
39	56	23.8	488	4	US-09-949-016-9120	Sequence 9120, Ap
40	56	23.8	851	1	US-08-369-796-2	Sequence 2, Appli
41	56	23.8	851	2	US-08-852-091-2	Sequence 2, Appli
42	56	23.8	851	2	US-08-820-754-2	Sequence 2, Appli
43	56	23.8	851	3	US-08-956-652-2	Sequence 2, Appli
44	56	23.8	851	3	US-08-956-652-2	Sequence 2, Appli
45	56	23.8	851	3	US-09-012-710-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-690-454-59
; Sequence 59, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59

Query Match 100.0%; Score 235; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-24;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPAPFRLWPIILGALSITFVLGLLSGFLVWRCRRRSSPPPX 44
Db 71 PPAPFRLWPIILGALSITFVLGLLSGFLVWRCRRRSSPPPX 114

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RESULT 2
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 44
   |||||
Db 71 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 3
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 44
   |||||
Db 71 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 44
   |||||
Db 71 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 5
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match      69.8%; Score 164; DB 4; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.5e-14;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSITFVLGSLGFLVWRCRRRSSPPPX 44
   |||||
Db 71 PPAHFRLLWPILGGALSITFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 6
US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
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;; PRIORITY APPLICATION NUMBER: 60/172,878
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: 60/203,347
;; PRIOR FILING DATE: 2000-05-10
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match 69.8%; Score 164; DB 4; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.5e-14;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGLSGFLVWRCRRRSPPPX 44
DB 71 PPAFRLWPILGGALSLVLVLSVFLVWRCRRRKKFTTPI 114

RESULT 7

US-09-949-016-6907
;; Sequence 6907, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6907
;; LENGTH: 365
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-6907

Query Match 26.8%; Score 63; DB 4; Length 365;
Best Local Similarity 45.9%; Pred. No. 2.1;
Matches 17; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 5 FRLWPILGGALSLTFVLGLSGFLVWRCRRRSS 40
DB 220 FR-FWPLVIVILSALFLGTACFCVWRRRKKQKS 255

RESULT 8

US-09-949-016-7325
;; Sequence 7325, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7325
;; LENGTH: 391
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7325

Query Match 26.8%; Score 63; DB 4; Length 391;
Best Local Similarity 45.9%; Pred. No. 2.2;
Matches 17; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 5 FRLWPILGGALSLTFVLGLSGFLVWRCRRRSS 40
DB 246 FR-FWPLVIVILSALFLGTACFCVWRRRKKQKS 281

RESULT 9

US-08-127-499A-1
;; Sequence 1, Application US/08127499A
;; Patent No. 5510264
;; GENERAL INFORMATION:
;; APPLICANT: VAN ALSTYNE, Diane
;; APPLICANT: SHARMA, Lawrence Rajendra
;; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
;; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/127,499A
;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/102/INBI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 992 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-08-127-499A-1

Query Match 26.0%; Score 61; DB 1; Length 992;
Best Local Similarity 38.8%; Pred. No. 12;
Matches 19; Conservative 6; Mismatches 16; Indels 8; Gaps 3;

QY 3 APFRLWPILGGALSL-----TFVLGLSGFLVWRCRR--ERSPPPX 44
DB 518 SPASALMLATANALSLDHAFAFVL-LVPWVLIFWVCRCRERRAPPPP 565

RESULT 10

US-08-482-947-1
;; Sequence 1, Application US/08482847
;; Patent No. 5556757
;; GENERAL INFORMATION:
;; APPLICANT: VAN ALSTYNE, Diane
;; APPLICANT: SHARMA, Lawrence Rajendra

;; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
;; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,847
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/127,499
;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/104/INBI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 992 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-08-482-847-1

Query Match 26.0%; Score 61; DB 1; Length 992;
Best Local Similarity 38.8%; Pred. No. 12;
Matches 19; Conservative 6; Mismatches 16; Indels 8; Gaps 3;
Qy 3 APFRLLPILGALSL-----TFVLGILSGFLVWRRCRR--ERSSPPEX 44
Db 518 SPASALWLTANALSLDRAFAFVL-IVPWVLIFWVCRRCRRPAPPP 565

RESULT 11
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PC/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7
Query Match 25.5%; Score 60; DB 4; Length 309;
Best Local Similarity 31.0%; Pred. No. 4.3;
Matches 13; Conservative 2; Mismatches 5; Indels 22; Gaps 1;
Qy 1 PPAPFRLLPILGALSLTFVLGILSGFLVWRRCRRSSPP 42
Db 71 PPAPFRL-----WRSCDKTHTCPP 90

RESULT 12
US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match 25.5%; Score 60; DB 4; Length 309;
Best Local Similarity 31.0%; Pred. No. 4.3;
Matches 13; Conservative 2; Mismatches 5; Indels 22; Gaps 1;
Qy 1 PPAPFRLLPILGALSLTFVLGILSGFLVWRRCRRSSPP 42
Db 71 PPAPFRL-----WRSCDKTHTCPP 90

RESULT 13
US-08-121-713D-58
; Sequence 58, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-713D-58

Query Match 25.5%; Score 60; DB 1; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGFLVWRCRRSSPPX 44
DB 639 GAL-----VVGFIGFLFSRRCRGEDYTDMPF 665

RESULT 14
US-08-835-268-58
Sequence 58, Application US/08835268
Patent No. 5807826
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-835-268-58

Query Match 25.5%; Score 60; DB 1; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;
QY 14 GALSITFVLGSLGFLVWRCRRSSPPX 44
DB 639 GAL-----VVGFIGFLFSRRCRGEDYTDMPF 665

RESULT 15
US-09-060-692-58
Sequence 58, Application US/09060692
Patent No. 5935865
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-692-58

Query Match 25.5%; Score 60; DB 2; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGFLVWRCRRSSPPX 44
DB 639 GAL-----VVGFIGFLFSRRCRGEDYTDMPF 665

Search completed: February 14, 2005, 07:24:52
Job time : 44 secs

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